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(54) Title: GERANYL DIPHOSPHATE SYNTHASE FROM MINT (<i>MENTHA PIPERITA</i>)		
(57) Abstract <p>A cDNA encoding geranyl diphosphate synthase from peppermint has been isolated and sequenced, and the corresponding amino acid sequence has been determined. Accordingly, an isolated DNA sequence (SEQ ID No: 1) is provided which codes for the expression of geranyl diphosphate synthase (SEQ ID No: 2) from peppermint (<i>Mentha piperita</i>). In other aspects, replicable recombinant cloning vehicles are provided which code for geranyl diphosphate synthase or for a base sequence sufficiently complementary to at least a portion of the geranyl diphosphate synthase DNA or RNA to enable hybridization therewith (e.g., antisense geranyl diphosphate synthase RNA or fragments of complementary geranyl diphosphate synthase DNA which are useful as polymerase chain reaction primers or as probes for geranyl diphosphate synthase or related genes). In yet other aspects, modified host cells are provided that have been transformed, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence encoding geranyl diphosphate synthase. Thus, systems and methods are provided for the recombinant expression of geranyl diphosphate synthase that may be used to facilitate the production, isolation and purification of significant quantities of recombinant geranyl diphosphate synthase for subsequent use, to obtain expression or enhanced expression of geranyl diphosphate synthase in plants in order to enhance the production of monoterpenoids, to produce geranyl diphosphate in cancerous cells as a precursor to monoterpenoids having anti-cancer properties or may be otherwise employed for the regulation or expression of geranyl diphosphate synthase or the production of geranyl diphosphate.</p>		

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GERANYL DIPHOSPHATE SYNTHASE FROM MINT (*Mentha piperita*)

Field of the Invention

The present invention relates to nucleic acid sequences which code for geranyl diphosphate synthases, such as geranyl diphosphate synthase from *Mentha piperita*,
5 and to vectors containing the sequences, host cells containing the sequences and methods of producing recombinant geranyl diphosphate synthases and their mutants.

Background of the Invention

Geranyl diphosphate synthase (GPP synthase) is one of a family of enzymes called prenyl transferases that catalyze C₅ elongation reactions to form the linear
10 (acyclic) precursors of the various terpenoid families. GPP synthase catalyzes the condensation of dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP) to form geranyl diphosphate (GPP) which is the immediate, C₁₀ acyclic precursor of the monoterpenes (Wise, M.L. and Croteau, R., in Cane, D.E., ed., "Comprehensive Natural Products Chemistry: Isoprenoids, Vol. 2", Elsevier Science,
15 Oxford, 1997 (in press)) (FIG. 1). Farnesyl diphosphate synthase (FPP synthase), a related prenyl transferase, utilizes GPP and IPP as substrates to form farnesyl diphosphate (FPP), which is the immediate, C₁₅ precursor of the sesquiterpenes (FIG. 1). Another prenyl transferase, geranylgeranyl diphosphate synthase (GGPP synthase), catalyzes the condensation of farnesyl diphosphate and IPP to form
20 geranylgeranyl diphosphate (GGPP) which is the immediate C₂₀ precursor of the diterpene family (FIG. 1). Other types of prenyl transferases can utilize GGPP and IPP as substrates to form very long chain molecules, such as natural rubber. Poulter C.D. and Rilling, H.C., *Accts. Chem. Res.* 11: 307-313 (1978); Scolnik, P.A. and Bartley, G., *Plant Mol. Biol. Rep.* 14: 305, 307 (1996).

The basic reaction mechanism for all of these prenyl transferases is the same, and consists of three steps (see FIG. 2 in which the reaction catalyzed by geranyl diphosphate synthase is presented as illustrative of the general reaction mechanism). With reference to FIGURE 2, in the first step an allylic diphosphate ester (2a) is
5 ionized to the stable carbonium ion (2b). The carbonium ion then attacks the double bond of isopentenyl diphosphate (2c) to yield another carbonium ion (2d). In the final step of the cycle, a proton is eliminated from the newly formed carbonium ion (2d) to form a terpenoid containing a new allylic double bond (2e). In the reaction catalyzed by GPP synthase, the allylic diphosphate ester is dimethyl allyl diphosphate (FIG. 1
10 and FIG. 2). In the reactions catalyzed by FPP synthase and GGPP synthase the allylic diphosphate ester is geranyl diphosphate and farnesyl diphosphate, respectively (FIG. 1).

Unlike FPP synthase and GGPP synthase, which produce GPP as an intermediate and which are nearly ubiquitous (Ogura, K. and Koyama, T., in Ogura, K. and Sankawa, U., eds., "Dynamic Aspects of Natural Products Chemistry"
15 Kodansha/Harwood Academic Publishers, Tokyo, pp. 1-23, 1997), geranyl diphosphate synthase is largely restricted to plant species that produce abundant quantities of monoterpenes. Because both FPP synthase and GGPP synthase produce only negligible levels of GPP as a free intermediate on route to FPP and GGPP
20 (Ogura, K. and Koyama, T., *supra*), it is geranyl diphosphate synthase that provides the crucial link between primary metabolism and monoterpene biosynthesis and that serves as the essential driver of monoterpene biosynthesis (Wise, M.L. and Croteau, R., *supra*).

Any attempt, therefore, to exploit recombinant methods to increase the yield
25 of monoterpene-producing (essential oil) species, or to genetically engineer the monoterpene biosynthetic pathway into any non-producing species (*e.g.*, field crops, fruit-bearing plant species and animals) requires access to a geranyl diphosphate synthase gene or cDNA clone. Co-expression of geranyl diphosphate synthase along with a selected monoterpene synthase, such as (-)-limonene synthase (Colby et al.,
30 *J. Biol. Chem.* 268:23016-23024, 1993), and any subsequent pathway enzymes, should allow production of the corresponding monoterpene product(s) from simple carbon substrates, such as glucose, in any living organism.

Monoterpenes are utilized as flavoring agents in food products, and as scents in perfumes (Arctander, S., in *Perfume and Flavor Materials of Natural Origin*,
35 Arctander Publications, Elizabeth, New Jersey; Bedoukian, P.Z. in *Perfumery and*

Flavoring Materials, 4th edition, Allured Publications, Wheaton, Illinois, 1995; Allured, S., in *Flavor and Fragrance Materials*, Allured Publications, Wheaton, Illinois, 1997. Monoterpenes are also used as intermediates in various industrial processes. Dawson, F.A., in *The Amazing Terpenes*, Naval Stores Rev., March/April, 5 6-12, 1994. Monoterpenes are also implicated in the natural defense systems of plants against pests and pathogens. Francke, W. in Muller, P.M. and Lamparsky, D., eds., *Perfumes: Art, Science and Technology*, Elsevier Applied Science, NY, NY, 61-99, 1991; Harborne, J.B., in Harborne, J.B. and Tomas-Barberan, F.A., eds., *Ecological Chemistry and Biochemistry of Plant Terpenoids*, Clarendon Press, Oxford, 399-426, 10 1991; Gershenzon, J and Croteau, R in Rosenthal, G.A. and Berenbaum, M.R., eds., *Herbivores: Their Interactions with Secondary Plant Metabolites*, Academic Press, San Diego, 168-220, 1991.

There is also substantial evidence that monoterpenes are effective in the prevention and treatment of cancer (Elson, C.E. and Yu, S.G., *J. Nutr.* **124**: 607-614, 15 1994.). Thus, for example, limonene, perrilyl alcohol and geraniol have each been shown to have chemotherapeutic activity against a very broad range of mammalian cancers (see, for example, (1) limonene, Elegbede et al., *Carcinogenesis* **5**:661-665, 1984; Elson et al., *Carcinogenesis* **9**:331-332, 1988; Maltzman et al., *Carcinogenesis* **10**:781-785, 1989; Wattenberg, L.W. and Coccia, J.B., *Carcinogenesis* **12**:115-117, 20 1991; Wattenberg, L.W. and Coccia, J.B., *Carcinogenesis* **12**:115-117, 1991; Haag et al., *Cancer Res.* **52**:4021-4026, 1992; Crowell, P.L. and Gould, M.N., *CRC Crit. Rev. Oncogenesis* **5**:1-22, 1994; (2) perillyl alcohol, Mills et al., *Cancer Res.* **55**:979-983, 1995; Haag, J.D. and Gould, M.N., *Cancer Chemother. Pharmacol.* **34**:477-483, 1994; Stark et al., *Cancer Lett.* **96**:15-21, 1995 and (3) geraniol, Shoff 25 et al., *Cancer Res.* **51**:37-42, 1991; Yu et al., *J. Nutr.* **125**:2763-2767, 1995; Burke et al., *Lipids* **32**:151-156, 1997.).

Cancer cells can be modified to produce therapeutic amounts of a monoterpene having anti-cancer properties by targeting the cognate monoterpene synthase protein to cancer cells, or by introducing a monoterpene synthase gene into 30 cancer cells. This approach to cancer therapy is complicated, however, by the fact that the natural distribution of geranyl diphosphate synthase is largely restricted to plant species that produce abundant quantities of monoterpenes. Thus, animal cells do not naturally produce the monoterpene precursor geranyl diphosphate. Consequently, the genetic manipulation of cancer cells to produce endogenous 35 monoterpenes having anti-cancer properties requires the introduction of a gene

encoding geranyl diphosphate synthase, together with a gene encoding a monoterpene synthase that produces a monoterpene having anti-cancer properties. Similarly, if the protein targeting approach is utilized, both geranyl diphosphate synthase protein and monoterpene synthase protein must be targeted to cancer cells.

- 5 Standard protein targeting techniques can be used to introduce geranyl diphosphate synthase along with a monoterpene synthase, such as limonene synthase (Colby et al., *J. Biol. Chem.* **268**:23016-23024, 1993), into animal cells with specific targeting to tumors. See, e.g., Wearley, L.L., *Critical Reviews in Therapeutic Drug Carrier Systems*, **8**(4): 331-394, 1991; Sheldon, K et al., *Proc. Nat'l. Acad. Sci. USA.*, **92**(6): 2056-2060, 1995. In addition, standard gene therapy techniques can be used to target a GPP synthase gene and a monoterpene synthase gene to cancerous cells for endogenous synthesis of monoterpenes having anti-cancer properties. For reviews of gene targeting technology see; Mahato R.I et al., *Pharmaceutical Research* **14**(7): 853-859, 1997; Rosenthal, F.M. and Mertelsmann, R., *Onkologie* **20**(1): 26-34, 1997; Buckel, P., *Trends in Pharmacological Sciences* **17**(12): 450-456, 1996; Roth, J.A. and Cristiano, R.J., *J. Nat'l Cancer Inst.* **89**(1): 21-39, 1997; Ledley, F.D, *Pharmaceutical Research* **13**(11): 1595-1614, 1996.

To date, extracts containing geranyl diphosphate synthase activity have been isolated from several plant sources, including grape (Clastre et al., *Plant Physiol.* **102**:205-211, 1993); geranium (Suga, T. and Endo, T., *Phytochemistry* **30**:1757-1761, 1991); sage (Croteau, R. and Purkett, P.T., *Arch. Biochem. Biophys.* **271**:524-535, 1989) and *Lithospermum* (Heide, L. and Berger, U., *Arch. Biochem. Biophys.* **273**:331-338, 1989). Only the enzyme from grape has been purified to homogeneity (Clastre et al., *supra*).

25 Table 1 summarizes the limited, available physical and chemical characteristics of geranyl diphosphate synthase isolated from several species.

TABLE 1

Deduced characteristics of geranyl diphosphate synthase^a

Native molecular weight	66 kDa(V), 70 kDa(M), 73 kDa(L), 100 kDa(S)
Subunit configuration	monomer(V), dimer(M)
Cofactor requirements	Divalent metal ions required for catalysis Mg^{2+} (M,S,L) or Mn^{2+} (P,V)
Apparent V_{max}	9.4 μ mol/min/mg(L) 150 nmol/h/mg(S)
Apparent K_m	IPP 14 μ M(L), 8.5 μ M(V), 7.3 μ M(S) DMAPP 83 μ M(L), 56.8 μ M(V), 5.6 μ M(S)
pH optimum	7.0(S), 6.75(L)
Isoelectric point	4.95(L) 5.42(M18)
Inhibitors	Thiol-directed reagents(S), aminophenylethyl diphosphate(V), geranyl diphosphate (L,M)
Catalytic enhancers under <i>in vitro</i> conditions	1% v/v Triton-X 100(P,V,M)

5 These data reveal that the physical and chemical properties of geranyl diphosphate synthase vary considerably between species. For example, molecular mass varies from 66 kDa (in grape) to 100 kDa (in sage). Similarly, the isoelectric point of geranyl diphosphate synthase isolated from *Lithospermum erythrorhizon* is 4.95, while the "pseudomature" form of mint geranyl diphosphate synthase (*i.e.*, the protein encoded

^a Geranyl diphosphate synthase characteristics are compiled from the data disclosed in: Croteau, R. and Purkett, P.T., *Arch. Biochem. Biophys.* 271: 524-535, 1989; Heide, L. and Berger, U., *Arch. Biochem. Biophys.* 273: 331-338, 1989; Suga, T. and Endo, T., *Phytochemistry* 30: 1757-1761, 1991; Clastre et al., *Plant Physiol.* 102: 205-211, 1993. Uppercase letters in parentheses designate the following species: (M) *Mentha spicata*, (V) *Vitis vinifera*, (L) *Lithospermum erythrorhizon*, (S) *Salvia officinalis*, (P) *Pelargonium roseum*. (M18) refers to the "pseudomature" form of the GPP synthase encoded by cDNA clone Mp13.18 from *Mentha piperita* as described at page 8, *supra*.

by the cDNA insert of clone Mp13.18 having the first 48 amino acids deleted from the amino terminus) has an isoelectric point of 5.42. This variation in the physical and chemical properties of geranyl diphosphate synthase isolated from different species is reflected in the fact that the published purification protocols are each significantly different from the others.

Amino acid sequence data for geranyl diphosphate synthase has not been reported in the art. Although several DNA sequences encoding plant-derived FPP synthases and GGPP synthases are available (Scolnik, P.A. and Bartley, G.E., *Plant Mol. Biol. Report* 14:305-319, 1996), no genes for geranyl diphosphate synthase have thus far been reported.

Summary of the Invention

In accordance with the foregoing, cDNAs encoding geranyl diphosphate synthase from peppermint have been isolated and sequenced, and the corresponding amino acid sequences have been deduced. Accordingly, the present invention relates to isolated, recombinant geranyl diphosphate synthase proteins, and portions thereof, to isolated DNA sequences which code for the expression of geranyl diphosphate synthase, and portions thereof, such as the sequence designated SEQ ID No:1 which encodes geranyl diphosphate synthase (SEQ ID No:2) from peppermint (*Mentha piperita*). In other aspects, the present invention is directed to replicable recombinant cloning vehicles comprising a nucleic acid sequence, e.g., a DNA sequence which codes for a geranyl diphosphate synthase or for a base sequence sufficiently complementary to at least a portion of the geranyl diphosphate synthase DNA or RNA to enable hybridization therewith (e.g., antisense geranyl diphosphate synthase RNA or fragments of complementary geranyl diphosphate synthase DNA which are useful as polymerase chain reaction primers or as probes for geranyl diphosphate synthase or related genes). In yet other aspects of the invention, modified host cells are provided that have been transformed, transfected, infected and/or injected with a recombinant cloning vehicle and/or DNA sequence of the invention. Thus, the present invention provides for the recombinant expression of geranyl diphosphate synthases. The inventive concepts described herein may be used to facilitate the production, isolation and purification of significant quantities of recombinant geranyl diphosphate synthase (or of the primary enzyme product, geranyl diphosphate) for subsequent use, to obtain expression or enhanced expression of geranyl diphosphate synthase in plants, microorganisms or animals, or may be otherwise employed in an

environment where the regulation or expression of geranyl diphosphate synthase is desired for the production of geranyl diphosphate synthase or the enzyme product, geranyl diphosphate, or its derivatives.

In yet another aspect of the present invention, methods are provided for treating cancer. The methods include the step of introducing a geranyl diphosphate synthase protein into a cancer cell, together with a monoterpene synthase protein that is capable of converting geranyl diphosphate to a monoterpene having anticancer properties. Alternatively, nucleic acid sequences encoding a geranyl diphosphate synthase protein and a monoterpene synthase protein, that is capable of converting geranyl diphosphate to a monoterpene having anticancer properties, are introduced into a cancer cell.

Brief Description of the Drawings

The foregoing aspects and many of the attendant advantages of this invention will be better understood by reference to the following detailed description, when taken in conjunction with the accompanying drawings, wherein:

FIGURE 1 shows the condensation reactions catalyzed by (a) geranyl diphosphate synthase, (b) farnesyl diphosphate synthase and (c) geranylgeranyl diphosphate synthase.

FIGURE 2 shows the reaction mechanism common to all prenyltransferases. The reaction catalyzed by geranyl diphosphate synthase is presented as illustrative of the general mechanism.

Detailed Description of the Preferred Embodiment

As used herein, the terms "amino acid" and "amino acids" refer to all naturally occurring L- α -amino acids or their residues. The amino acids are identified by either the single-letter or three-letter designations:

Asp	D	aspartic acid	Ile	I	isoleucine
Thr	T	threonine	Leu	L	leucine
Ser	S	serine	Tyr	Y	tyrosine
Glu	E	glutamic acid	Phe	F	phenylalanine
Pro	P	proline	His	H	histidine
Gly	G	glycine	Lys	K	lysine
Ala	A	alanine	Arg	R	arginine
Cys	C	cysteine	Trp	W	tryptophan

Val	V	valine	Gln	Q	glutamine
Met	M	methionine	Asn	N	asparagine

As used herein, the term "nucleotide" means a monomeric unit of DNA or RNA containing a sugar moiety (pentose), a phosphate and a nitrogenous heterocyclic base. The base is linked to the sugar moiety via the glycosidic carbon (1' carbon of pentose) and that combination of base and sugar is called a nucleoside. The base characterizes the nucleotide with the four bases of DNA being adenine ("A"), guanine ("G"), cytosine ("C") and thymine ("T"). Inosine ("I") is a synthetic base that can be used to substitute for any of the four, naturally-occurring bases (A, C, G or T). The four RNA bases are A, G, C and uracil ("U"). The nucleotide sequences described herein comprise a linear array of nucleotides connected by phosphodiester bonds between the 3' and 5' carbons of adjacent pentoses.

The term "percent identity" (%I) means the percentage of amino acids or nucleotides that occupy the same relative position when two amino acid sequences, or two nucleic acid sequences, are aligned side by side.

The term "percent similarity" (%S) is a statistical measure of the degree of relatedness of two compared protein sequences. The percent similarity is calculated by a computer program that assigns a numerical value to each compared pair of amino acids based on chemical similarity (e.g., whether the compared amino acids are acidic, basic, hydrophobic, aromatic, etc.) and/or evolutionary distance as measured by the minimum number of base pair changes that would be required to convert a codon encoding one member of a pair of compared amino acids to a codon encoding the other member of the pair. Calculations are made after a best fit alignment of the two sequences has been made empirically by iterative comparison of all possible alignments. (Henikoff, S. and Henikoff, J.G., *Proc. Nat'l Acad Sci USA* **89**: 10915-10919, 1992).

As set forth herein, the percent identity and percent similarity values, at the amino acid level, between the *Mentha* GPP synthase disclosed herein (SEQ ID No:2) and GGPP synthases are averages of the values obtained from individual, pairwise comparisons made between the deduced amino acid sequence of the *Mentha* GPP synthase disclosed herein (SEQ ID No:2) and the GGPP synthases set forth in Table 2. Similarly, as set forth herein, the percent identity and percent similarity values, at the amino acid level, between the *Mentha* GPP synthase disclosed herein (SEQ ID No:2) and FPP synthases are averages of the values obtained from individual, pairwise comparisons made between the deduced amino acid sequence of the *Mentha* GPP

synthase disclosed herein (SEQ ID No:2) and the FPP synthases set forth in Table 2. The %I and %S values set forth in Table 2 are the values obtained from the individual, pairwise comparisons of the *Mentha* GPP synthase protein sequence (SEQ ID No: 2) and each of the sequences listed in Table 2.

5

Table 2

Monoterpene Synthase	Species	Accession Number	%S	%I
GGPP Synthase	Capsicum annum	X80267	54	30
GGPP synthase	Catharanthus roseus	X92893	56	29
GGPP synthase	Arabidopsis thaliana	L25813	53	26
FPP synthase	Zea mays	L39789	41	17
FPP synthase	Lupinus albus	U15777	38	15

10 %S means the percent similarity with the deduced amino acid sequence of the *Mentha* GPP synthase disclosed herein (SEQ ID No:2). %I means the percent identity with the deduced amino acid sequence of the *Mentha* GPP synthase disclosed herein (SEQ ID No:2). Accession numbers refer to the accession numbers for the GenBank sequence database.

15 "Oligonucleotide" refers to short length single or double stranded sequences of deoxyribonucleotides linked via phosphodiester bonds. The oligonucleotides are chemically synthesized by known methods and purified, for example, on polyacrylamide gels.

The term "geranyl diphosphate synthase" is used herein to mean an enzyme capable of catalyzing the condensation of dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP) to form geranyl diphosphate, the immediate acyclic precursor of the monoterpenes, as described herein.

20 The term "essential oil plant," or "essential oil plants," refers to a group of plant species that produce high levels of monoterpene and/or sesquiterpene and/or diterpene oils, and/or high levels of monoterpene and/or sesquiterpene and/or diterpene resins. The foregoing oils and/or resins account for greater than about 0.005% of the fresh weight of an essential oil plant that produces them. The essential oils and/or resins are more fully described, for example, in E. Guenther, The Essential Oils, Vols. I-VI, R.E. Krieger Publishing Co., Huntington N.Y., 1975, incorporated herein by reference. The essential oil plants include, but are not limited to:

25 Lamiaceae, including, but not limited to, the following species: Ocimum (basil), Lavandula (Lavender), Origanum (oregano), Mentha (mint), Salvia (sage), Rosmarinus (rosemary), Thymus (thyme), Satureja and Monarda.

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Umbelliferae, including, but not limited to, the following species: Carum (caraway), Anethum (dill), feniculum (fennel) and Daucus (carrot).

Asteraceae (Compositae), including, but not limited to, the following species: Artemisia (tarragon, sage brush), Tanacetum (tansy).

5 Rutaceae (e.g., citrus plants); Rosaceae (e.g., roses); Myrtaceae (e.g., eucalyptus, Melaleuca); the Gramineae (e.g., Cymbopogon (citronella)); Geranaceae (Geranium) and certain conifers including Abies (e.g., Canadian balsam), Cedrus (cedar) and Thuja and Juniperus.

10 The range of essential oil plants is more fully set forth in *E. Guenther, The Essential Oils, Vols. I-VI, R.E. Krieger Publishing Co., Huntington N.Y., 1975*, which is incorporated herein by reference.

The term "angiosperm" refers to a class of plants that produce seeds that are enclosed in an ovary.

15 The term "gymnosperm" refers to a class of plants that produce seeds that are not enclosed in an ovary.

The terms "alteration", "amino acid sequence alteration", "variant" and "amino acid sequence variant" refer to geranyl diphosphate synthase molecules with some differences in their amino acid sequences as compared to native geranyl diphosphate synthase. Ordinarily, the variants will possess at least about 70% homology with native geranyl diphosphate synthase, and preferably they will be at least about 80% homologous with native geranyl diphosphate synthase. The amino acid sequence variants of geranyl diphosphate synthase falling within this invention possess substitutions, deletions, and/or insertions at certain positions. Sequence variants of geranyl diphosphate synthase may be used to attain desired enhanced or reduced enzymatic activity, modified regiochemistry or stereochemistry, or altered substrate utilization or product distribution.

25 Substitutional geranyl diphosphate synthase variants are those that have at least one amino acid residue in the native geranyl diphosphate synthase sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule. Substantial changes in the activity of the geranyl diphosphate synthase molecule may be obtained by substituting an amino acid with a side chain that is significantly different in charge and/or structure from that of the native amino acid. This type of substitution would be expected to affect the structure

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of the polypeptide backbone and/or the charge or hydrophobicity of the molecule in the area of the substitution.

Moderate changes in the activity of the geranyl diphosphate synthase molecule would be expected by substituting an amino acid with a side chain that is similar in charge and/or structure to that of the native molecule. This type of substitution, referred to as a conservative substitution, would not be expected to substantially alter either the structure of the polypeptide backbone or the charge or hydrophobicity of the molecule in the area of the substitution.

Insertional geranyl diphosphate synthase variants are those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in the native geranyl diphosphate synthase molecule. Immediately adjacent to an amino acid means connected to either the α -carboxy or α -amino functional group of the amino acid. The insertion may be one or more amino acids. Ordinarily, the insertion will consist of one or two conservative amino acids. Amino acids similar in charge and/or structure to the amino acids adjacent to the site of insertion are defined as conservative. Alternatively, this invention includes insertion of an amino acid with a charge and/or structure that is substantially different from the amino acids adjacent to the site of insertion.

Deletional variants are those where one or more amino acids in the native geranyl diphosphate synthase molecule have been removed. Ordinarily, deletional variants will have one or two amino acids deleted in a particular region of the geranyl diphosphate synthase molecule.

The terms "biological activity", "biologically active", "activity" and "active," when used with reference to geranyl diphosphate synthase, refer to the ability of the geranyl diphosphate synthase molecule to condense dimethylallyl diphosphate (DMAPP) and isopentenyl diphosphate (IPP) to form geranyl diphosphate, as measured in an enzyme activity assay, such as the assay described in Example 1 below. Amino acid sequence variants of geranyl diphosphate synthase may have desirable altered biological activity including, for example, altered reaction kinetics, substrate utilization product distribution or other characteristics such as regiochemistry and stereochemistry.

The terms "DNA sequence encoding", "DNA encoding" and "nucleic acid encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order

of amino acids along the translated polypeptide chain. The DNA sequence thus codes for the amino acid sequence.

The terms "replicable expression vector" and "expression vector" refer to a piece of DNA, usually double-stranded, which may have inserted into it a piece of foreign DNA. Foreign DNA is defined as heterologous DNA, which is DNA not naturally found in the host. The vector is used to transport the foreign or heterologous DNA into a suitable host cell. Once in the host cell, the vector can replicate independently of or coincidental with the host chromosomal DNA, and several copies of the vector and its inserted (foreign) DNA may be generated. In addition, the vector contains the necessary elements that permit translating the foreign DNA into a polypeptide. Many molecules of the polypeptide encoded by the foreign DNA can thus be rapidly synthesized.

The terms "transformed host cell," "transformed" and "transformation" refer to the introduction of DNA into a cell. The cell is termed a "host cell", and it may be a prokaryotic or a eukaryotic cell. Typical prokaryotic host cells include various strains of *E. coli*. Typical eukaryotic host cells are plant cells, such as maize cells, yeast cells, insect cells or animal cells. The introduced DNA is usually in the form of a vector containing an inserted piece of DNA. The introduced DNA sequence may be from the same species as the host cell or from a different species from the host cell, or it may be a hybrid DNA sequence, containing some foreign DNA and some DNA derived from the host species.

In accordance with the present invention, a cDNA encoding geranyl diphosphate synthase was isolated and sequenced in the following manner. Geranyl diphosphate synthase is located exclusively in the glandular trichome secretory cells and catalyzes the formation of geranyl diphosphate in these essential oil species. These secretory cell clusters were isolated from *Mentha spicata* by known methods and geranyl diphosphate synthase was purified therefrom utilizing a novel purification protocol consisting of a dye-ligand chromatography step, and an anion exchange chromatography step followed by preparative SDS-PAGE. The limited amount of purified geranyl diphosphate synthase yielded the sequence of a nine amino acid peptide (SEQ. ID. No:3). This sequence information was insufficient to permit a reverse genetic approach to cloning the geranyl diphosphate synthase cDNA, *i.e.*, there was insufficient amino acid sequence to permit the construction of degenerate oligonucleotide probes that were sufficiently specific to be effective as probes.

Consequently, total RNA was extracted from isolated trichome secretory cells derived from *Mentha piperita* and mRNA was purified therefrom. The secretory cell mRNA served as the substrate for the synthesis of a cDNA library by standard means. One hundred, randomly selected cDNA clones were sequenced and one clone showed
5 low homology to plant-derived geranylgeranyl diphosphate synthases (~28% identity; ~54% similarity). Sequence information derived from this "prenyltransferase-like" cDNA was used to construct PCR primers (SEQ ID No:4 and SEQ ID No:5) which were, in turn, used to amplify a 113 bp fragment (SEQ ID No:6) of the "prenyltransferase-like" cDNA which was used as a probe to isolate twenty seven
10 additional, homologous clones from the glandular trichome, secretory cell library. Sequencing revealed that the twenty seven clones represented three alleles. The biological activity of one clone from each of the three allele groups was tested by measuring geranyl diphosphate activity in supernatant derived from *E. coli* individually expressing each of the three, representative cDNAs. The clone showing
15 the highest level of geranyl diphosphate synthase activity (designated Mp13.18) was completely sequenced (SEQ ID No:1) and its identity as a geranyl diphosphate synthase clone was confirmed by comparing the deduced geranyl diphosphate synthase protein sequence with the sequence of the nine amino acid peptide (SEQ ID No:3) derived from geranyl diphosphate synthase protein purified from *Mentha*
20 *spicata*.

Additionally, the sequence of an eight amino acid peptide (SEQ ID No:7), derived from geranyl diphosphate synthase protein purified from *Mentha spicata*, was obtained subsequent to the cloning of geranyl diphosphate synthase. The sequences of both the nine amino acid peptide (SEQ ID No:3), and the eight amino acid peptide
25 (SEQ ID No:7) exactly matched the corresponding regions of the protein sequence deduced from the cloned geranyl diphosphate synthase cDNA (SEQ ID No:2, amino acids 254 thru 262, and 184 thru 191, respectively). The observation that the peptide sequences derived from purified *Mentha spicata* geranyl diphosphate synthase perfectly matched the corresponding regions of the cloned *Mentha piperita* geranyl
30 diphosphate synthase is consistent with the genetic relationship between the two species: peppermint (*Mentha piperita*) is a hexaploid species produced by crossing *Mentha aquatica* with tetraploid *Mentha spicata* (Harley and Brighton, *Bot. J. Linn. Soc.* 74:71-96 [1977]). In effect, hexaploid peppermint contains the complete genome of tetraploid spearmint.

The isolation of the geranyl diphosphate synthase cDNA permits the development of an efficient expression system for this functional enzyme; provides a useful tool for examining the developmental regulation of monoterpene biosynthesis and permits the isolation of other geranyl diphosphate synthases. The isolation of the
5 geranyl diphosphate synthase cDNA also permits the transformation of a wide range of organisms in order to introduce monoterpene biosynthesis *de novo*, or to modify endogenous monoterpene biosynthesis.

Although the geranyl diphosphate synthase protein set forth in SEQ ID No:2 directs the enzyme to plastids, substitution of the putative targeting sequence
10 (SEQ ID No:2, amino acids 1 to 48) with other transport sequences well known in the art (see, e.g., von Heijne G et al., *Eur. J. Biochem* 180: 535-545, 1989; Stryer, *Biochemistry* W.H. Freeman and Company, New York, NY, p. 769 [1988]) may be employed to direct the geranyl diphosphate synthase to other cellular or extracellular locations.

15 In addition to the native geranyl diphosphate synthase amino acid sequence of SEQ ID No:2 encoded by the cDNA insert of plasmid Mp 13.18 (SEQ ID No:1), sequence variants produced by deletions, substitutions, mutations and/or insertions are intended to be within the scope of the invention except insofar as limited by the prior art. Geranyl diphosphate synthase amino acid sequence variants may be
20 constructed by mutating the DNA sequence that encodes wild-type geranyl diphosphate synthase, such as by using techniques commonly referred to as site-directed mutagenesis. Various polymerase chain reaction (PCR) methods now well known in the field, such as a two primer system like the Transformer Site-Directed Mutagenesis kit from Clontech, may be employed for this purpose.

25 Following denaturation of the target plasmid in this system, two primers are simultaneously annealed to the plasmid; one of these primers contains the desired site-directed mutation, the other contains a mutation at another point in the plasmid resulting in elimination of a restriction site. Second strand synthesis is then carried out, tightly linking these two mutations, and the resulting plasmids are transformed
30 into a *mutS* strain of *E. coli*. Plasmid DNA is isolated from the transformed bacteria, restricted with the relevant restriction enzyme (thereby linearizing the unmutated plasmids), and then retransformed into *E. coli*. This system allows for generation of mutations directly in an expression plasmid, without the necessity of subcloning or generation of single-stranded phagemids. The tight linkage of the two mutations and
35 the subsequent linearization of unmutated plasmids results in high mutation efficiency

and allows minimal screening. Following synthesis of the initial restriction site primer, this method requires the use of only one new primer type per mutation site. Rather than prepare each positional mutant separately, a set of "designed degenerate" oligonucleotide primers can be synthesized in order to introduce all of the desired mutations at a given site simultaneously. Transformants can be screened by sequencing the plasmid DNA through the mutagenized region to identify and sort mutant clones. Each mutant DNA can then be restricted and analyzed by electrophoresis on Mutation Detection Enhancement gel (J.T. Baker) to confirm that no other alterations in the sequence have occurred (by band shift comparison to the unmutagenized control).

The verified mutant duplexes can be cloned into a replicable expression vector, if not already cloned into a vector of this type, and the resulting expression construct used to transform *E. coli*, such as strain *E. coli* BL21(DE3)pLysS, for high level production of the mutant protein, and subsequent purification thereof. The method of FAB-MS mapping can be employed to rapidly check the fidelity of mutant expression. This technique provides for sequencing segments throughout the whole protein and provides the necessary confidence in the sequence assignment. In a mapping experiment of this type, protein is digested with a protease (the choice will depend on the specific region to be modified since this segment is of prime interest and the remaining map should be identical to the map of unmutagenized protein). The set of cleavage fragments is fractionated by microbore HPLC (reversed phase or ion exchange, again depending on the specific region to be modified) to provide several peptides in each fraction, and the molecular weights of the peptides are determined by FAB-MS. The masses are then compared to the molecular weights of peptides expected from the digestion of the predicted sequence, and the correctness of the sequence quickly ascertained. Since this mutagenesis approach to protein modification is directed, sequencing of the altered peptide should not be necessary if the MS agrees with prediction. If necessary to verify a changed residue, CAD-tandem MS/MS can be employed to sequence the peptides of the mixture in question, or the target peptide purified for subtractive Edman degradation or carboxypeptidase Y digestion depending on the location of the modification.

In the design of a particular site directed mutant, it is generally desirable to first make a non-conservative substitution (e.g., Ala for Cys, His or Glu) and determine if activity is greatly impaired as a consequence. The properties of the mutagenized protein are then examined with particular attention to the kinetic

parameters of K_m and k_{cat} as sensitive indicators of altered function, from which changes in binding and/or catalysis *per se* may be deduced by comparison to the native enzyme. If the residue is by this means demonstrated to be important by activity impairment, or knockout, then conservative substitutions can be made, such as Asp for Glu to alter side chain length, Ser for Cys, or Arg for His. For hydrophobic segments, it is largely size that will be altered, although aromatics can also be substituted for alkyl side chains. Changes in the normal product distribution can indicate which step(s) of the reaction sequence have been altered by the mutation.

Other site directed mutagenesis techniques may also be employed with the nucleotide sequences of the invention. For example, restriction endonuclease digestion of DNA followed by ligation may be used to generate geranyl diphosphate synthase deletion variants, as described in section 15.3 of Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York, NY [1989]). A similar strategy may be used to construct insertion variants, as described in section 15.3 of Sambrook et al., *supra*.

Oligonucleotide-directed mutagenesis may also be employed for preparing substitution variants of this invention. It may also be used to conveniently prepare the deletion and insertion variants of this invention. This technique is well known in the art as described by Adelman et al. (*DNA* 2:183 [1983]). Generally, oligonucleotides of at least 25 nucleotides in length are used to insert, delete or substitute two or more nucleotides in the geranyl diphosphate synthase molecule. An optimal oligonucleotide will have 12 to 15 perfectly matched nucleotides on either side of the nucleotides coding for the mutation. To mutagenize the wild-type geranyl diphosphate synthase, the oligonucleotide is annealed to the single-stranded DNA template molecule under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of *E. coli* DNA polymerase I, is then added. This enzyme uses the oligonucleotide as a primer to complete the synthesis of the mutation-bearing strand of DNA. Thus, a heteroduplex molecule is formed such that one strand of DNA encodes the wild-type geranyl diphosphate synthase inserted in the vector, and the second strand of DNA encodes the mutated form of geranyl diphosphate synthase inserted into the same vector. This heteroduplex molecule is then transformed into a suitable host cell.

Mutants with more than one amino acid substituted may be generated in one of several ways. If the amino acids are located close together in the polypeptide chain, they may be mutated simultaneously using one oligonucleotide that codes for

all of the desired amino acid substitutions. If however, the amino acids are located some distance from each other (separated by more than ten amino acids, for example) it is more difficult to generate a single oligonucleotide that encodes all of the desired changes. Instead, one of two alternative methods may be employed. In the first method, a separate oligonucleotide is generated for each amino acid to be substituted. The oligonucleotides are then annealed to the single-stranded template DNA simultaneously, and the second strand of DNA that is synthesized from the template will encode all of the desired amino acid substitutions. An alternative method involves two or more rounds of mutagenesis to produce the desired mutant. The first round is as described for the single mutants: wild-type geranyl diphosphate synthase DNA is used for the template, an oligonucleotide encoding the first desired amino acid substitution(s) is annealed to this template, and the heteroduplex DNA molecule is then generated. The second round of mutagenesis utilizes the mutated DNA produced in the first round of mutagenesis as the template. Thus, this template already contains one or more mutations. The oligonucleotide encoding the additional desired amino acid substitution(s) is then annealed to this template, and the resulting strand of DNA now encodes mutations from both the first and second rounds of mutagenesis. This resultant DNA can be used as a template in a third round of mutagenesis, and so on.

The gene encoding geranyl diphosphate synthase may be incorporated into any organism (intact plant, animal, microbe), or cell culture derived therefrom, that produces dimethylallyl diphosphate and isopentenyl diphosphate to effect the conversion of these primary substrates to geranyl diphosphate and its subsequent metabolic products, depending on the organism. The geranyl diphosphate synthase gene may be introduced into any organism for a variety of purposes including, but not limited to: production or modification of flavor and aroma properties; improvement of defense capability; the alteration of other ecological interactions mediated by geranyl diphosphate and its derivatives; selective destruction or inhibition of the growth, development or division of cancerous cells; or the production of geranyl diphosphate and its derivatives.

Eukaryotic expression systems may be utilized for geranyl diphosphate synthase production since they are capable of carrying out any required posttranslational modifications and of directing the enzyme to the proper membrane location. A representative eukaryotic expression system for this purpose uses the recombinant baculovirus, *Autographa californica* nuclear polyhedrosis virus

(AcNPV; M.D. Summers and G.E. Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures* [1986]; Luckow et al., *Bio-technology* 6:47-55 [1987]) for expression of the geranyl diphosphate synthase of the invention. Infection of insect cells (such as cells of the species *Spodoptera frugiperda*) with the recombinant baculoviruses allows for the production of large amounts of the geranyl diphosphate synthase protein. In addition, the baculovirus system has other important advantages for the production of recombinant geranyl diphosphate synthase. For example, baculoviruses do not infect humans and can therefore be safely handled in large quantities. In the baculovirus system, a DNA construct is prepared including a DNA segment encoding geranyl diphosphate synthase and a vector. The vector may comprise the polyhedron gene promoter region of a baculovirus, the baculovirus flanking sequences necessary for proper cross-over during recombination (the flanking sequences comprise about 200-300 base pairs adjacent to the promoter sequence) and a bacterial origin of replication which permits the construct to replicate in bacteria. The vector is constructed so that (i) the DNA segment is placed adjacent (or operably linked or "downstream" or "under the control of") to the polyhedron gene promoter and (ii) the promoter/geranyl diphosphate synthase combination is flanked on both sides by 200-300 base pairs of baculovirus DNA (the flanking sequences).

To produce the geranyl diphosphate synthase DNA construct, a cDNA clone encoding the full length geranyl diphosphate synthase is obtained using methods such as those described herein. The DNA construct is contacted in a host cell with baculovirus DNA of an appropriate baculovirus (that is, of the same species of baculovirus as the promoter encoded in the construct) under conditions such that recombination is effected. The resulting recombinant baculoviruses encode the full geranyl diphosphate synthase. For example, an insect host cell can be cotransfected or transfected separately with the DNA construct and a functional baculovirus. Resulting recombinant baculoviruses can then be isolated and used to infect cells to effect production of the geranyl diphosphate synthase. Host insect cells include, for example, *Spodoptera frugiperda* cells, that are capable of producing a baculovirus-expressed geranyl diphosphate synthase. Insect host cells infected with a recombinant baculovirus of the present invention are then cultured under conditions allowing expression of the baculovirus-encoded geranyl diphosphate synthase. Geranyl diphosphate synthase thus produced is then extracted from the cells using methods known in the art.

Other eukaryotic microbes such as yeasts may also be used to practice this invention. The baker's yeast *Saccharomyces cerevisiae*, is a commonly used yeast, although several other strains are available. The plasmid YRp7 (Stinchcomb et al., *Nature* 282:39 [1979]; Kingsman et al., *Gene* 7:141 [1979]; Tschemper et al., *Gene* 10:157 [1980]) is commonly used as an expression vector in *Saccharomyces*. This plasmid contains the *trp1* gene that provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, such as strains ATCC No. 44,076 and PEP4-1 (Jones, *Genetics* 85:12 [1977]). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan. Yeast host cells are generally transformed using the polyethylene glycol method, as described by Hinnen (*Proc. Natl. Acad. Sci. USA* 75:1929 [1978]). Additional yeast transformation protocols are set forth in Gietz et al., *N.A.R.* 20(17):1425, 1992; Reeves et al., *FEMS* 99:193-197, 1992.

Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073 [1980]) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149 [1968]; Holland et al., *Biochemistry* 17:4900 [1978]), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triose-phosphate isomerase, phosphoglucose isomerase, and glucokinase. In the construction of suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination. Other promoters that have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing yeast-compatible promoter, origin of replication and termination sequences is suitable.

Cell cultures derived from multicellular organisms, such as plants, may be used as hosts to practice this invention. Transgenic plants can be obtained, for example, by transferring plasmids that encode geranyl diphosphate synthase and a selectable marker gene, e.g., the *kan* gene encoding resistance to kanamycin, into *Agrobacterium tumefaciens* containing a helper Ti plasmid as described in

Hoeckema et al., *Nature* 303:179-181 [1983] and culturing the *Agrobacterium* cells with leaf slices of the plant to be transformed as described by An et al., *Plant Physiology* 81:301-305 [1986]. Transformation of cultured plant host cells is normally accomplished through *Agrobacterium tumefaciens*, as described above.

5 Cultures of mammalian host cells and other host cells that do not have rigid cell membrane barriers are usually transformed using the calcium phosphate method as originally described by Graham and Van der Eb (*Virology* 52:546 [1978]) and modified as described in sections 16.32-16.37 of Sambrook et al., *supra*. However, other methods for introducing DNA into cells such as Polybrene (Kawai and

10 Nishizawa, *Mol. Cell. Biol.* 4:1172 [1984]), protoplast fusion (Schaffner, *Proc. Natl. Acad. Sci. USA* 77:2163 [1980]), electroporation (Neumann et al., *EMBO J.* 1:841 [1982]), and direct microinjection into nuclei (Capecchi, *Cell* 22:479 [1980]) may also be used. Additionally, animal transformation strategies are reviewed in Monastersky G.M. and Robl, J.M., *Strategies in Transgenic Animal Science*, ASM

15 Press, Washington, D.C., 1995. Transformed plant calli may be selected through the selectable marker by growing the cells on a medium containing, e.g., kanamycin, and appropriate amounts of phytohormone such as naphthalene acetic acid and benzyladenine for callus and shoot induction. The plant cells may then be regenerated and the resulting plants transferred to soil using techniques well known to those

20 skilled in the art.

In addition, a gene regulating geranyl diphosphate synthase production can be incorporated into the plant along with a necessary promoter which is inducible. In the practice of this embodiment of the invention, a promoter that only responds to a specific external or internal stimulus is fused to the target cDNA. Thus, the gene will

25 not be transcribed except in response to the specific stimulus. As long as the gene is not being transcribed, its gene product is not produced.

An illustrative example of a responsive promoter system that can be used in the practice of this invention is the glutathione-S-transferase (GST) system in maize. GSTs are a family of enzymes that can detoxify a number of hydrophobic electrophilic

30 compounds that often are used as pre-emergent herbicides (Weigand et al., *Plant Molecular Biology* 7:235-243 [1986]). Studies have shown that the GSTs are directly involved in causing this enhanced herbicide tolerance. This action is primarily mediated through a specific 1.1 kb mRNA transcription product. In short, maize has a naturally occurring quiescent gene already present that can respond to external

35 stimuli and that can be induced to produce a gene product. This gene has previously

been identified and cloned. Thus, in one embodiment of this invention, the promoter is removed from the GST responsive gene and attached to a geranyl diphosphate synthase gene that previously has had its native promoter removed. This engineered gene is the combination of a promoter that responds to an external chemical stimulus
5 and a gene responsible for successful production of geranyl diphosphate synthase.

In addition to the methods described above, several methods are known in the art for transferring cloned DNA into a wide variety of plant species, including gymnosperms, angiosperms, monocots and dicots (see, e.g., Glick and Thompson, eds., *Methods in Plant Molecular Biology*, CRC Press, Boca Raton,
10 Florida [1993], incorporated by reference herein). Representative examples include electroporation-facilitated DNA uptake by protoplasts in which an electrical pulse transiently permeabilizes cell membranes, permitting the uptake of a variety of biological molecules, including recombinant DNA (Rhodes et al., *Science*,
240:204-207 [1988]); treatment of protoplasts with polyethylene glycol (Lyznik et al.,
15 *Plant Molecular Biology*, 13:151-161 [1989]); and bombardment of cells with DNA-laden microprojectiles which are propelled by explosive force or compressed gas to penetrate the cell wall (Klein et al., *Plant Physiol.* 91:440-444 [1989] and Boynton et al., *Science*, 240:1534-1538 [1988]). Transformation of *Taxus* species can be achieved, for example, by employing the methods set forth in Han et al, *Plant*
20 *Science*, 95:187-196 (1994), incorporated by reference herein. A method that has been applied to Rye plants (*Secale cereale*) is to directly inject plasmid DNA, including a selectable marker gene, into developing floral tillers (de la Pena et al., *Nature* 325:274-276 (1987)). Further, plant viruses can be used as vectors to transfer genes to plant cells. Examples of plant viruses that can be used as vectors to
25 transform plants include the Cauliflower Mosaic Virus (Brisson et al., *Nature* 310: 511-514 (1984); Additionally, plant transformation strategies and techniques are reviewed in Birch, R.G., *Ann Rev Plant Phys Plant Mol Biol*, 48:297 (1997); Forester et al., *Exp. Agric.*, 33:15-33 (1997). The aforementioned publications disclosing plant transformation techniques are incorporated herein by reference, and
30 minor variations make these technologies applicable to a broad range of plant species.

Each of these techniques has advantages and disadvantages. In each of the techniques, DNA from a plasmid is genetically engineered such that it contains not only the gene of interest, but also selectable and screenable marker genes. A selectable marker gene is used to select only those cells that have integrated copies of
35 the plasmid (the construction is such that the gene of interest and the selectable and

screenable genes are transferred as a unit). The screenable gene provides another check for the successful culturing of only those cells carrying the genes of interest. A commonly used selectable marker gene is neomycin phosphotransferase II (NPT II). This gene conveys resistance to kanamycin, a compound that can be added directly to the growth media on which the cells grow. Plant cells are normally susceptible to kanamycin and, as a result, die. The presence of the NPT II gene overcomes the effects of the kanamycin and each cell with this gene remains viable. Another selectable marker gene which can be employed in the practice of this invention is the gene which confers resistance to the herbicide glufosinate (Basta). A screenable gene commonly used is the β -glucuronidase gene (GUS). The presence of this gene is characterized using a histochemical reaction in which a sample of putatively transformed cells is treated with a GUS assay solution. After an appropriate incubation, the cells containing the GUS gene turn blue. Preferably, the plasmid will contain both selectable and screenable marker genes.

The plasmid containing one or more of these genes is introduced into either plant protoplasts or callus cells by any of the previously mentioned techniques. If the marker gene is a selectable gene, only those cells that have incorporated the DNA package survive under selection with the appropriate phytotoxic agent. Once the appropriate cells are identified and propagated, plants are regenerated. Progeny from the transformed plants must be tested to insure that the DNA package has been successfully integrated into the plant genome.

Mammalian host cells may also be used in the practice of the invention. Examples of suitable mammalian cell lines include monkey kidney CVI line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line 293S (Graham et al., *J. Gen. Virol.* 36:59 [1977]); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells (Urlab and Chasin, *Proc. Natl. Acad. Sci USA* 77:4216 [1980]); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243 [1980]); monkey kidney cells (CVI-76, ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor cells (MMT 060562, ATCC CCL 51); rat hepatoma cells (HTC, MI 54, Baumann et al., *J. Cell Biol.* 85:1 [1980]); and TRI cells (Mather et al., *Annals N.Y. Acad. Sci.* 383:44 [1982]). Expression vectors for these cells ordinarily include (if necessary) DNA sequences for

an origin of replication, a promoter located in front of the gene to be expressed, a ribosome binding site, an RNA splice site, a polyadenylation site, and a transcription terminator site.

Promoters used in mammalian expression vectors are often of viral origin. 5 These viral promoters are commonly derived from polyoma virus, Adenovirus 2, and most frequently Simian Virus 40 (SV40). The SV40 virus contains two promoters that are termed the early and late promoters. These promoters are particularly useful because they are both easily obtained from the virus as one DNA fragment that also contains the viral origin of replication (Fiers et al., *Nature* 273:113 [1978]). 10 or larger SV40 DNA fragments may also be used, provided they contain the approximately 250-bp sequence extending from the HindIII site toward the BglII site located in the viral origin of replication.

Alternatively, promoters that are naturally associated with the foreign gene (homologous promoters) may be used provided that they are compatible with the host 15 cell line selected for transformation.

An origin of replication may be obtained from an exogenous source, such as SV40 or other virus (e.g., Polyoma, Adeno, VSV, BPV) and inserted into the cloning vector. Alternatively, the origin of replication may be provided by the host cell 20 chromosomal replication mechanism. If the vector containing the foreign gene is integrated into the host cell chromosome, the latter is often sufficient.

The use of a secondary DNA coding sequence can enhance production levels of geranyl diphosphate synthase in transformed cell lines. The secondary coding sequence typically comprises the enzyme dihydrofolate reductase (DHFR). The wild-type form of DHFR is normally inhibited by the chemical methotrexate (MTX). The 25 level of DHFR expression in a cell will vary depending on the amount of MTX added to the cultured host cells. An additional feature of DHFR that makes it particularly useful as a secondary sequence is that it can be used as a selection marker to identify transformed cells. Two forms of DHFR are available for use as secondary sequences, wild-type DHFR and MTX-resistant DHFR. The type of DHFR used in a particular 30 host cell depends on whether the host cell is DHFR deficient (such that it either produces very low levels of DHFR endogenously, or it does not produce functional DHFR at all). DHFR-deficient cell lines such as the CHO cell line described by Urlaub and Chasin, *supra*, are transformed with wild-type DHFR coding sequences. After transformation, these DHFR-deficient cell lines express functional DHFR and

are capable of growing in a culture medium lacking the nutrients hypoxanthine, glycine and thymidine. Nontransformed cells will not survive in this medium.

The MTX-resistant form of DHFR can be used as a means of selecting for transformed host cells in those host cells that endogenously produce normal amounts of functional DHFR that is MTX sensitive. The CHO-K1 cell line (ATCC No. CL 61) possesses these characteristics, and is thus a useful cell line for this purpose. The addition of MTX to the cell culture medium will permit only those cells transformed with the DNA encoding the MTX-resistant DHFR to grow. The nontransformed cells will be unable to survive in this medium.

Prokaryotes may also be used as host cells for the initial cloning steps of this invention. They are particularly useful for rapid production of large amounts of DNA, for production of single-stranded DNA templates used for site-directed mutagenesis, for screening many mutants simultaneously, and for DNA sequencing of the mutants generated. Suitable prokaryotic host cells include *E. coli* K12 strain 294 (ATCC No. 31,446), *E. coli* strain W3110 (ATCC No. 27,325) *E. coli* X1776 (ATCC No. 31,537), and *E. coli* B; however many other strains of *E. coli*, such as HB101, JM101, NM522, NM538, NM539, and many other species and genera of prokaryotes including bacilli such as *Bacillus subtilis*, other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may all be used as hosts. Prokaryotic host cells or other host cells with rigid cell walls are preferably transformed using the calcium chloride method as described in section 1.82 of Sambrook et al., *supra*. Alternatively, electroporation may be used for transformation of these cells. Prokaryote transformation techniques are set forth in Dower, W. J., in Genetic Engineering, Principles and Methods, 12:275-296, Plenum Publishing Corp., 1990; Hanahan et al., *Meth. Enzymol.*, 204:63, 1991.

As a representative example, cDNA sequences encoding geranyl diphosphate synthase may be transferred to the (His)₆-Tag pET vector commercially available (from Novagen) for overexpression in *E. coli* as heterologous host. This pET expression plasmid has several advantages in high level heterologous expression systems. The desired cDNA insert is ligated in frame to plasmid vector sequences encoding six histidines followed by a highly specific protease recognition site (thrombin) that are joined to the amino terminus codon of the target protein. The histidine "block" of the expressed fusion protein promotes very tight binding to immobilized metal ions and permits rapid purification of the recombinant protein by immobilized metal ion affinity chromatography. The histidine leader sequence is then

cleaved at the specific proteolysis site by treatment of the purified protein with thrombin, and the geranyl diphosphate synthase again purified by immobilized metal ion affinity chromatography, this time using a shallower imidazole gradient to elute the recombinant synthase while leaving the histidine block still adsorbed. This overexpression-purification system has high capacity, excellent resolving power and is fast, and the chance of a contaminating *E. coli* protein exhibiting similar binding behavior (before and after thrombin proteolysis) is extremely small.

As will be apparent to those skilled in the art, any plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell may also be used in the practice of the invention. The vector usually has a replication site, marker genes that provide phenotypic selection in transformed cells, one or more promoters, and a polylinker region containing several restriction sites for insertion of foreign DNA. Plasmids typically used for transformation of *E. coli* include pBR322, pUC18, pUC19, pUC118, pUC119, and Bluescript M13, all of which are described in sections 1.12-1.20 of Sambrook et al., *supra*. However, many other suitable vectors are available as well. These vectors contain genes coding for ampicillin and/or tetracycline resistance which enables cells transformed with these vectors to grow in the presence of these antibiotics.

The promoters most commonly used in prokaryotic vectors include the β -lactamase (penicillinase) and lactose promoter systems (Chang et al. *Nature* 375:615 [1978]; Itakura et al., *Science* 198:1056 [1977]; Goeddel et al., *Nature* 281:544 [1979]) and a tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057 [1980]; EPO Appl. Publ. No. 36,776), and the alkaline phosphatase systems. While these are the most commonly used, other microbial promoters have been utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally into plasmid vectors (see Siebenlist et al., *Cell* 20:269 [1980]).

Many eukaryotic proteins normally secreted from the cell contain an endogenous secretion signal sequence as part of the amino acid sequence. Thus, proteins normally found in the cytoplasm can be targeted for secretion by linking a signal sequence to the protein. This is readily accomplished by ligating DNA encoding a signal sequence to the 5' end of the DNA encoding the protein and then expressing this fusion protein in an appropriate host cell. The DNA encoding the signal sequence may be obtained as a restriction fragment from any gene encoding a protein with a signal sequence. Thus, prokaryotic, yeast, and eukaryotic signal

sequences may be used herein, depending on the type of host cell utilized to practice the invention. The DNA and amino acid sequence encoding the signal sequence portion of several eukaryotic genes including, for example, human growth hormone, proinsulin, and proalbumin are known (see Stryer, *Biochemistry* W.H. Freeman and Company, New York, NY, p. 769 [1988]), and can be used as signal sequences in appropriate eukaryotic host cells. Yeast signal sequences, as for example acid phosphatase (Arima et al., *Nuc. Acids Res.* 11:1657 [1983]), alpha-factor, alkaline phosphatase and invertase may be used to direct secretion from yeast host cells. Prokaryotic signal sequences from genes encoding, for example, LamB or OmpF (Wong et al., *Gene* 68:193 [1988]), MalE, PhoA, or beta-lactamase, as well as other genes, may be used to target proteins from prokaryotic cells into the culture medium.

The geranyl diphosphate synthase protein having the sequence set forth in SEQ ID NO:2 includes an amino terminal membrane insertion sequence at residues 1 through 48, and in the embodiment shown in SEQ ID No:2 directs the enzyme to plastids. Alternative trafficking sequences from plants, animals and microbes can be employed in the practice of the invention to direct the gene product to the cytoplasm, endoplasmic reticulum, mitochondria or other cellular components, or to target the protein for export to the medium. These considerations apply to the overexpression of geranyl diphosphate synthase, and to direction of expression within cells or intact organisms to permit gene product function in any desired location.

The construction of suitable vectors containing DNA encoding replication sequences, regulatory sequences, phenotypic selection genes and the geranyl diphosphate synthase DNA of interest are prepared using standard recombinant DNA procedures. Isolated plasmids and DNA fragments are cleaved, tailored, and ligated together in a specific order to generate the desired vectors, as is well known in the art (see, for example, Sambrook et al., *supra*).

As discussed above, geranyl diphosphate synthase variants are preferably produced by means of mutation(s) that are generated using the method of site-specific mutagenesis. This method requires the synthesis and use of specific oligonucleotides that encode both the sequence of the desired mutation and a sufficient number of adjacent nucleotides to allow the oligonucleotide to stably hybridize to the DNA template.

In another aspect of the invention, the gene encoding geranyl diphosphate synthase may be introduced into cancerous cells in combination with a gene encoding a monoterpene synthase that produces a monoterpene having anti-cancer properties.

A geranyl diphosphate synthase gene must be introduced into cancerous cells, in addition to a gene encoding a monoterpene synthase producing a monoterpene having anti-cancer properties, because animal cells do not naturally produce geranyl diphosphate which is the chemical precursor to the monoterpenes. Examples of
5 monoterpenes having anti-cancer properties are limonene, perillyl alcohol and geraniol, as discussed at page 4, *supra*. Examples of nucleic acid sequences that encode monoterpene synthases are disclosed in the following, copending patent applications, each of which is incorporated herein by reference: U.S. Patent Application Serial Number 08/846,526 "DNA Encoding Limonene Synthase from
10 *Mentha spicata*"; U.S. Patent Application Serial Number 08/937,540 "Monoterpene Synthases from Common Sage (*Salvia officinalis*) and PCT Patent Application Serial Number PCT/US98/14528 "Monoterpene Synthases from Grand fir (*Abies grandis*)."

Several methods are known in the art for the introduction of genes into human cells. For example, cell-based therapy can be used to introduce genes into cells while
15 they are outside of the body. Cell-based approaches involve removing cells from a patient, introducing genes encoding a therapeutic protein into the removed cells, and returning the cells to the patient by cell transplantation or transfusion. The cell-based approach has been used to treat Severe Combined Immune Deficiency (SCID), which is due to inherited defects in the enzyme adenosine deaminase (ADA). The gene
20 therapy treatment of SCID involved removal of peripheral blood lymphocytes or bone marrow progenitor cells from affected individuals, introduction of the normal ADA gene into the chromosomes of these cells using retroviral vectors, and reintroduction of the genetically engineered cells to the patient (C. Bordignon et al. *Science* 270:470, 474 (1995), R.M. Blaese et al., *Science* 270:475-479 (1995); D.B. Kohn et al.,
25 *Nature Med.* 1:1017-1023 (1995)). Initial results demonstrated that the genetically engineered cells will persist for prolonged periods of time, and that low level expression of ADA can be established.

Analogous cell-based approaches have been used to treat familial hypercholesterolemia (LDL-receptor deficiency) (M. Grossman et al., *Nature*
30 *Genetics* 6:335 41 (1994); M. Grossman et al., *Nature Med.* 1:1148-1154 (1995)) and Gaucher disease (J.A. Nolte et al., *J. Clin. Invest.* 90:342-348 (1992); L. Xu et al., *Exptl. Hematol.* 22:223-230 (1994); T. Ohashi et al., *Proc. Natl. Acad. Sci. USA.* 89:11332-11336 (1992)).

Genes can be introduced into cells *in situ*, or after removal of the cells from
35 the body, by means of viral vectors. For example, retroviruses are RNA viruses that

have the ability to insert their genes into host cell chromosomes after infection. Retroviral vectors have been developed that lack the genes encoding viral proteins, but retain the ability to infect cells and insert their genes into the chromosomes of the target cell (A.D. Miller, *Hum. Gen. Ther.* 1:5-14 (1990)). Retroviruses will only
5 efficiently infect dividing cells, thus when retroviruses are used to introduce genes into cells that have been removed from the body, cell division is stimulated with growth-promoting media or specific factors. *In vivo* application of retroviruses has been achieved by administration of virus-producing cells directly into tumors. Virus particle released by the infected cell will infect adjacent tumor cells, hence only a
10 relatively small percentage of cells in a tumor need be initially infected in order to ultimately introduce the targeted gene into most or all of the tumor cells. (K.W. Culver et al., *Science* 256:1550-1552 (1992)).

Adenoviral vectors are designed to be administered directly to patients. Unlike retroviral vectors, adenoviral vectors do not integrate into the chromosome of
15 the host cell. Instead, genes introduced into cells using adenoviral vectors are maintained in the nucleus as an extrachromosomal element (episome) that persists for a limited time period. Adenoviral vectors will infect dividing and non-dividing cells in many different tissues *in vivo* including airway epithelial cells, endothelial cells, hepatocytes and various tumors (B.C. Trapnell, *Adv Drug Del Rev.* 12:185-199
20 (1993)).

Another viral vector is the herpes simplex virus, a large, double-stranded DNA virus that has been used in some initial applications to deliver therapeutic genes to neurons and could potentially be used to deliver therapeutic genes to some forms of brain cancer (D.S. Latchman, *Mol. Biotechnol.* 2:179-95 (1994)). Recombinant
25 forms of the vaccinia virus can accommodate large inserts and are generated by homologous recombination. To date, this vector has been used to deliver interleukins (ILs), such as human IL-1 β and the costimulatory molecules B7-1 and B7-2 (G.R. Peplinski et al., *Ann. Surg. Oncol.* 2:151-9 (1995); J.W. Hodge et al., *Cancer Res.* 54:5552-55 (1994)).

Another approach to gene therapy involves the direct introduction of DNA plasmids into patients. (F.D. Ledley, *Hum. Gene Ther.* 6:1129-1144 (1995)). The plasmid DNA is taken up by cells within the body and can direct expression of recombinant proteins. Typically plasmid DNA is delivered to cells in the form of liposomes in which the DNA is associated with one or more lipids, such as DOTMA
35 (1,2-diolcylxypropyl-3-trimethyl ammonium bromide) and DOPE

(dioleoylphosphatidylethanolamine). Formulations with DOTMA have been shown to provide expression in pulmonary epithelial cells in animal models (K.L. Brigham et al., *Am. J. Med. Sci.*, **298**:278-281 (1989); A.B. Canonico et al., *Am. J. Respir. Cell. Mol. Biol.* **10**:24-29 (1994)). Additionally, studies have demonstrated that intramuscular
5 injection of plasmid DNA formulated with 5% PVP (50,000 kDa) increases the level of reporter gene expression in muscle as much as 200-fold over the levels found with injection of DNA in saline alone (R.J. Mumper et al., *Pharm. Res.* **13**:701-709 (1996); R.J. Mumper et al., *Proc. Intern. Symp. Cont. Rol. Bioac. Mater.* **22**:325-326 (1995)). Intramuscular administration of plasmid DNA results in gene expression that
10 lasts for many months (J.A. Wolff et al., *Hum. Mol. Genet.* **1**:363-369 (1992); M. Manthorpe et al., *Hum. Gene Ther.* **4**:419-431 (1993); G. Ascadi et al., *New Biol.* **3**:71-81 (1991), D. Gal et al., *Lab. Invest.* **68**:18-25 (1993)).

Additionally, uptake and expression of DNA has also been observed after direct injection of plasmid into the thyroid (M. Sikes et al., *Hum. Gene Ther.*
15 **5**:837-844 (1994)) and synovium (J. Yovandich et al., *Hum. Gene Ther.* **6**:603-610 (1995)). Lower levels of gene expression have been observed after interstitial injection into liver (M.A. Hickman et al., *Hum. Gene Ther.* **5**:1477-1483 (1994)), skin (E. Raz et al., *Proc. Natl. Acad. Sci.* **91**:9519-9523 (1994)), instillation into the airways (K.B. Meyer et al., *Gene Therapy* **2**:450-460 (1995)), application to the
20 endothelium (G.D. Chapman et al., *Circulation Res.* **71**:27-33 (1992); R. Riessen et al., *Human Gene Therapy*, **4**:749-758 (1993)), and after intravenous administration (R.M. Conry et al., *Cancer Res.* **54**:1164-1168 (1994)).

Various devices have been developed for enhancing the availability of DNA to the target cell. A simple approach is to contact the target cell physically with
25 catheters or implantable materials containing DNA (G.D. Chapman et al., *Circulation Res.* **71**:27-33 (1992)). Another approach is to utilize needle-free, jet injection devices which project a column of liquid directly into the target tissue under high pressure. (P.A. Furth et al., *Anal Biochem.* **20**:365-368 (1992); (H.L. Vahlsing et al., *J. Immunol. Meth.* **175**:11-22 (1994); (F.D. Ledley et al., *Cell Biochem.* **18A**:226 (1994)).
30

Another device for gene delivery is the "gene gun" or Biolistic™, a ballistic device that projects DNA-coated micro-particles directly into the nucleus of cells *in vivo*. Once within the nucleus, the DNA dissolves from the gold or tungsten microparticle and can be expressed by the target cell. This method has been used
35 effectively to transfer genes directly into the skin, liver and muscle (N.S. Yang et al.,

Proc. Natl. Acad. Sci. 87:9568-9572 (1990); L. Cheng et al., *Proc. Natl. Acad. Sci. USA* 90:4455-4459 (1993); R.S. Williams et al., *Proc. Natl. Acad. Sci.* 88:2726-2730 (1991)).

Another approach to targeted gene delivery is the use of molecular conjugates, which consist of protein or synthetic ligands to which a nucleic acid- or DNA-binding agent has been attached for the specific targeting of nucleic acids to cells (R.J. Cristiano et al., *Proc. Natl. Acad. Sci. USA* 90:11548-52 (1993); B.A. Bunnell et al., *Somat. Cell Mol. Genet.* 18:559-69 (1992); M. Cotten et al., *Proc. Natl. Acad. Sci. USA* 89:6094-98 (1992)). Once the DNA is coupled to the molecular conjugate, a protein-DNA complex results. This gene delivery system has been shown to be capable of targeted delivery to many cell types through the use of different ligands (R.J. Cristiano et al., *Proc. Natl. Acad. Sci. USA* 90:11548-52 (1993)). For example, the vitamin folate has been used as a ligand to promote delivery of plasmid DNA into cells that overexpress the folate receptor (e.g., ovarian carcinoma cells) (S. Gottschalk et al., *Gene Ther.* 1:185-91 (1994)). The malaria circumsporozoite protein has been used for the liver-specific delivery of genes under conditions in which ASOR receptor expression on hepatocytes is low, such as in cirrhosis, diabetes, and hepatocellular carcinoma (Z. Ding et al., *J. Biol. Chem.* 270:3667-76 (1995)). The overexpression of receptors for epidermal growth factor (EGF) on cancer cells has allowed for specific uptake of EGF/DNA complexes by lung cancer cells (R. Cristiano et al., *Cancer Gene Ther.* 3:4-10 (1996)).

Targeted expression of genes encoding proteins having anti-cancer activity can be achieved by placing the transgene under the control of an inducible promoter. For example, the promoter for the carcinoembryonic antigen (CEA) gene has been incorporated in vectors and it has directed cell-specific expression of the resulting CEA-expression vector constructs in tumors cells, such as those of pancreatic carcinoma (J.M. DiMaio et al., *Surgery* 116:205-13 (1994)). The regulatory sequences of the human surfactant protein A gene have been used to generate cell-specific expression in non-small-cell lung cancers that express this protein (M.J. Smith et al., *Hum. Gene Ther.* 5:29-35 (1994)).

Another approach to introducing geranyl diphosphate synthase protein, and monoterpene synthase protein, into a cancerous cell is to directly introduce the purified protein into the body. Typically, the protein is introduced in association with another molecule, such as a lipid, to protect the protein from enzymatic degradation. For example, the covalent attachment of polymers, especially polyethylene glycol

(PEG), has been used to protect certain proteins from enzymatic hydrolysis in the body and thus prolong half-life (F. Fuertges, et al., *J. Controlled Release*, **11**:139 (1990)). Many polymer systems have been reported for protein delivery (Y.H. Bae, et al., *J. Controlled Release*, **9**:271 (1989); R. Hori, et al., *Pharm. Res.*, **6**:813 (1989); I. Yamakawa, et al., *J. Pharm. Sci.*, **79**:505 (1990); I. Yoshihiro, et al., *J. Controlled Release*, **10**:195 (1989); M. Asano, et al., *J. Controlled Release*, **9**:111 (1989); J. Rosenblatt et al., *J. Controlled Release*, **9**:195 (1989); K. Makino, *J. Controlled Release*, **12**:235 (1990); Y. Takakura et al., *J. Pharm. Sci.*, **78**:117 (1989); Y. Takakura et al., *J. Pharm. Sci.*, **78**:219 (1989)).

Therapeutic proteins can be introduced into the body by application to a bodily membrane capable of absorbing the protein, for example the nasal, gastrointestinal and rectal membranes. The protein is typically applied to the absorptive membrane in conjunction with a permeation enhancer. (V.H.L. Lee, *Crit. Rev. Ther. Drug Carrier Syst.*, **5**:69 (1988); V.H.L. Lee, *J. Controlled Release*, **13**:213 (1990); V.H.L. Lee, Ed., *Peptide and Protein Drug Delivery*, Marcel Dekker, New York (1991); A.G. DeBoer et al., *J. Controlled Release*, **13**:241 (1990)). For example, STDHF is a synthetic derivative of fusidic acid, a steroidal surfactant that is similar in structure to the bile salts, and has been used as a permeation enhancer for nasal delivery. (W.A. Lee, *Biopharm.* Nov./Dec., **22**, 1990).

Additionally, microspheres bearing therapeutic protein can be delivered to the body. In one application, a bioadhesive was used to hold microspheres bearing protein in place in the nasal passages. When an absorption enhancer was incorporated into the microsphere with the protein, bioavailability was increased (L. Illum, et al., *Int. J. Pharm.*, **63**:207 (1990); N.F. Farraj et al., *J. Controlled Release*, **13**:253 (1990)).

The foregoing may be more fully understood in connection with the following representative examples, in which "Plasmids" are designated by a lower case p followed by an alphanumeric designation. The starting plasmids used in this invention are either commercially available, publicly available on an unrestricted basis, or can be constructed from such available plasmids using published procedures. In addition, other equivalent plasmids are known in the art and will be apparent to the ordinary artisan.

"Digestion", "cutting" or "cleaving" of DNA refers to catalytic cleavage of the DNA with an enzyme that acts only at particular locations in the DNA. These enzymes are called restriction endonucleases, and the site along the DNA sequence

where each enzyme cleaves is called a restriction site. The restriction enzymes used in this invention are commercially available and are used according to the instructions supplied by the manufacturers. (See also sections 1.60-1.61 and sections 3.38-3.39 of Sambrook et al., *supra*.)

5 "Recovery" or "isolation" of a given fragment of DNA from a restriction digest means separation of the resulting DNA fragment on a polyacrylamide or an agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of
10 the gel from DNA. This procedure is known generally. For example, see Lawn et al. (*Nucleic Acids Res.* 9:6103-6114 (1982)), and Goeddel et al. (*Nucleic Acids Res.*, *supra*).

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention. All
15 literature citations herein are expressly incorporated by reference.

EXAMPLES

Example 1

Geranyl Diphosphate Synthase Isolation

The purification strategy for *Mentha* geranyl diphosphate synthase was
20 developed empirically. The teachings of the prior art were inconsistent and could not be adapted for use in the isolation of geranyl diphosphate synthase from *Mentha*. For example, Clastre et al, *supra*, provides the only example in the art of completely purified geranyl diphosphate synthase (from grape). The purification protocol of Clastre et al consisted of the following steps: ammonium sulfate precipitation, anion
25 exchange chromatography (DEAE and Mono Q), hydroxyapatite chromatography, hydrophobic (phenyl-substituted) chromatography, gel permeation chromatography and non-denaturing polyacrylamide gel electrophoresis. Clastre et al reported that ammonium sulfate precipitation was the most efficient purification step. In contrast, in the purification of *Mentha* geranyl diphosphate synthase, reported herein, the
30 techniques of ammonium sulfate precipitation, hydroxyapatite chromatography, hydrophobic (phenyl-substituted) chromatography and gel permeation chromatography all failed. In particular, ammonium sulfate precipitation was particularly inefficient when applied to the isolation of *Mentha* geranyl diphosphate

synthase. Consequently, the following purification protocol was developed empirically.

Plant materials, substrates and reagents. Mint plants (*Mentha spicata*) were propagated and grown as previously described (Alonso et al., *J. Biol. Chem.* 267:7582-7587, 1992). Newly emerged, rapidly expanding leaves (5-10 mm long) of vegetative stems (3-7 weeks old) were used for the preparation of glandular trichome cells for enzyme purification (Gershenzon et al., *Anal. Biochem.* 200:130-138, 1992). [4-¹⁴C]Isopentenyl diphosphate (54 Ci/mol) was purchased from DuPont/NEN. Dimethylallyl diphosphate was synthesized as described (Davisson et al., *Methods Enzymol.* 110:130-144, 1985).

Assay for prenyltransferase activity. To 10 µl of enzyme solution was added 90 µl MOPSO buffer (25 mM, pH 7.0) containing 10% glycerol, 10 mM MgCl₂, and 1 mM DTT. DMAPP (10 µM) and [4-¹⁴C]IPP (7 µM) were added to initiate the reaction, and the contents were overlaid with 1 ml hexane. The mixture was vortexed briefly and then incubated for 1 h at 31°C. After incubation, 10 µl of 3 N HCl was added, the contents vortexed and centrifuged, and hydrolysis of the products was continued for 20 min at 31°C. After hydrolysis was complete, the reaction mixture was again vortexed and centrifuged so that the products derived from the acid labile allylic diphosphates (or those alcohols derived from hydrolysis by endogenous phosphatases) were partitioned into the hexane layer. The hexane was removed and the radioactive products contained therein were measured by liquid scintillation counting.

Product identification. For the identification of reaction products, the assay was scaled up by a factor of ten and pentane was substituted for the hexane overlay to improve recovery. After acid hydrolysis and removal of the pentane layer as described above, the reaction mixture was extracted with 2 x 1 ml of diethyl ether to ensure complete recovery of products. The combined organic extract was then dried over anhydrous Na₂SO₄ and concentrated to 100 µl, followed by addition of internal standards and further concentration for radio-GLC analysis. The products sought were: from farnesyl diphosphate, all *trans*-farnesol from endogenous phosphatase-catalyzed hydrolysis and *cis,trans*-farnesol and nerolidol from acid-catalyzed rearrangement (total C₁₅ alcohols); from geranyl diphosphate, geraniol from endogenous phosphatase-catalyzed hydrolysis and nerol and linalool from acid-catalyzed rearrangement (total C₁₀ alcohols); and total C₅ alcohols (dimethylallyl alcohol, isopentenol and dimethylvinyl carbinol).

Initial Preparation of Mint Glandular Trichome Extract Containing Geranyl Diphosphate Synthase. Glandular trichome cell clusters (approximately 2×10^7) were isolated from 40 g of leaf tissue following procedures previously described (Gershenzon et al., *Anal. Biochem.* 200:130-138, 1992). The isolated cell clusters
5 were suspended in KPi buffer (50 ml, 100 mM, pH 7.4, containing 5 g XAD, 0.5 g PVPP, 250 mM sucrose, 1 mM DTT, 1 mM PMSF and 1 mM Na_4EDTA), and were disrupted by sonication (Braun-sonic 2000, full power, five 15 s bursts separated by 45 s cooling in ice). The sonicate was filtered through a 20 μm nylon mesh and the filtrate was brought to 100 ml by the addition of 50 ml KPi buffer without XAD or
10 PVPP. The sonicate was then centrifuged at 18,000g (30 min), then at 195,000g (90 min), and the supernatant was utilized as the enzyme source.

Dye-ligand interaction chromatography. The supernatant combined from two gland preparations (200 ml) was dialyzed (2x, 4°C, 18 h total) in Mes buffer (4 l, 25 mM, pH 6.2) containing 10% glycerol, 1 mM DTT, and 10 mM MgCl_2 . The
15 dialyzed supernatant was equally divided into 8 (50 ml) polypropylene tubes containing 5 ml of DyeMatrex Red A Gel (Amicon) equilibrated with dialysis buffer in each tube. After 1 h of gentle mixing (Labquake), the contents were poured into eight 1.5 x 12 cm polypropylene columns (Bio-Rad), gravity drained, and washed with 4x volumes of dialysis buffer. Geranyl diphosphate synthase was then eluted
20 with Bis-Tris buffer (240 ml, 25 mM, pH 7.0) containing 10% glycerol, 5 mM KPi, 1 mM DTT, and 1 mM EDTA. The entire procedure was performed at 0-4°C.

Anion exchange chromatography. The elutant from the dye-ligand interaction chromatography step was loaded on to an HR 10/10 column containing Source 15Q separation media (Pharmacia Biotech) equilibrated in Bis-Tris buffer A (25 mM, pH
25 7.0) containing 10% glycerol and 1 mM DTT. Geranyl diphosphate synthase was eluted with a gradient (0-400 mM KCl in buffer A; total volume 400 ml). The highest activity fractions were collected (6 ml) and stored at -80°C. Farnesyl diphosphate synthase eluted at 4-10 mM KCl; geranyl diphosphate synthase eluted at 140-180 mM KCl; geranylgeranyl diphosphate synthase activity was not detected. Anion exchange
30 chromatography afforded the most significant purification step for geranyl diphosphate synthase.

To identify the geranyl diphosphate synthase protein in the anion exchange chromatography fractions, equal volumes from each fraction containing geranyl diphosphate activity were loaded onto an SDS-PAGE gel and the proteins contained
35 therein were resolved and silver stained. The correlation of protein stain intensity

with geranyl diphosphate synthase activity level in each fraction allowed the identification of a well resolved 29 kDa band as the target enzyme. Additional evidence was provided by calibrated gel permeation chromatography (Superdex 75) which indicated that the geranyl diphosphate synthase eluted at volumes
5 corresponding to ~70 kDa (major) and ~30 kDa, consistent with a 70 kDa homodimeric native enzyme that yields 30 kDa subunits which retain at least some catalytic activity.

Preparative SDS-PAGE. The partially purified geranyl diphosphate synthase from the anion chromatography step (60 ml) was heated to 95°C for 15 min, cooled,
10 and dialyzed in distilled water (2x, 4 l, 18 h, 4°C). The protein solution was then lyophilized to a powder and suspended in 100 µl of SDS buffer plus 50 µl of 3x loading buffer and separated by SDS-PAGE on 12.5% acrylamide at 35 mA for 6 h [15 cm x 18 cm x 1.5 mm gel] by a standard protocol (Laemmli, U.K., *Nature* 227:680-685, 1970). Coomassie Blue staining revealed ten protein bands, with the
15 most prominent band corresponding to 29 kDa and estimated at 10µg protein, based upon calibrated staining intensity with carbonic anhydrase as reference. The 29 kDa protein band, that was coincident with geranyl diphosphate synthase activity on ion exchange chromatography, was excised from the gel and combined in a microcentrifuge tube.

Amino acid analysis and protein sequencing. The presumptive geranyl diphosphate synthase protein (approximately 10 µg) contained in the SDS-PAGE gel slice was digested with trypsin (Promega V511/1,2) following published protocols (Coligan, J.E. in Coligan et al., eds. "Current Protocols in Protein Science, Vol. 1," John Wiley and Sons, New York, 11.3.1-11.3.13, 1996). The peptide mixture was
25 then loaded onto an Applied Biosystems C18 column (Aquapure ODS-300) which was equilibrated with distilled water/1% trifluoroacetic acid (TFA) (buffer A) and separated by gradient elution with buffer B consisting of 70% CH₃CN, 29% distilled water, and 1% TFA (0-60 min, 0%-37% buffer B/ 60-90 min, 37%-75% buffer B/ 90-105 min, 75%-100% buffer B). Five resolvable peptides were subjected to amino-
30 terminal sequence analysis via Edman degradation at the Washington State University Laboratory for Biotechnology and Bioanalysis. Two of the five digestion products yielded unambiguous peptide sequences; FGLYQGTLR (SEQ ID No:3) and RVIEISR (SEQ ID No:7). The other peptides collected yielded no useful sequence information, either because of low recovery or due to the presence of contaminants.

Example 2

Cloning of Geranyl Diphosphate Synthase cDNA

Shotgun cloning and sequencing. Since further scale-up of the geranyl diphosphate synthase purification protocol was impractical, the limited geranyl diphosphate synthase peptide sequence information precluded an exclusively sequence-based cloning strategy. Consequently, a random sequencing effort was initiated from a highly enriched source, i.e., a cDNA library constructed from mRNA isolated from peppermint oil gland cells that constitute the exclusive source of monoterpene biosynthesis in *Mentha*.

Mint plants (*Mentha piperita*) were propagated and grown as previously described (Alonso et al., *J. Biol. Chem.* 267:7582-7587, 1992). Secretory cells were isolated from 5-day-old peppermint leaves (Gershenzon et al., *Anal. Biochem.* 200:130-138, 1992), and total RNA was extracted from the isolated secretory cells (Logemann et al., *Anal. Biochem.* 163: 16-20, 1987). Poly(A)⁺-RNA was purified by chromatography on oligo(dT)-cellulose (Pharmacia), and 5 µg of the resulting mRNA were utilized to construct a λZAP cDNA library according to the manufacturer's instructions (Stratagene). Plasmids were purified from a mass excision of mint gland λZAPII phagemids (Stratagene). The plasmids were sequenced (DyeDeoxy Terminator Cycle Sequencing, Applied Biosystems) using the T3 promoter primer and the data subsequently acquired on the ABI sequenator. The NCBI BLAST server was used for database searching using the programs of the GCG Wisconsin package (Genetics Computer Group, 1994 Program Manual for the Wisconsin Package, Version 8, Genetics Computer Group, Madison, WI.).

Within the first one hundred clones sequenced, one promising clone (Mp10:13) was found to be "prenyltransferase-like" in sequence, in that it showed low homology to plant-derived geranylgeranyl diphosphate synthases (~28% identity; ~54% similarity) but little homology to plant-derived farnesyl diphosphate synthases (~ 16% identity; ~ 40% similarity). The PCR primers pMp13F (SEQ ID No:4) and pMp13R (SEQ ID No:5), derived from the sequence of clone Mp10:13, were used to amplify a 113 bp, 5'-fragment (SEQ ID No:6) which was labeled using the same primers and α³²P-dATP. The resulting probe was used to screen 3000 mint gland library λZAPII cDNA clones at high stringency. The filters bearing the 3000 λZAPII cDNA clones were hybridized with the radiolabelled, 113 bp probe overnight at 42°C in 30% formaldehyde, 5X SSPE (0.75 M NaCl, 0.05M NaH₂PO₄, 0.005M EDTA at

pH 7.4), 5x Denhardt's Reagent (0.1% Ficoll 400, 0.1% polyvinylpyrrolidone, 0.1% bovine serum albumin), 0.1% SDS and 20µg/ml denatured, sheared herring sperm DNA. The filters were then washed three times, for thirty minutes per wash, in 1x SSC (0.15M NaCl and 0.0165M sodium citrate) and 0.1% SDS at 65°C. Twenty-seven positive clones were purified through a second round of screening and were sequenced with T3 and T7 promoter primers. Sequencing revealed that the cloned genes represented three alleles.

Assay of the Biological Activity of the Proteins Encoded by the Putative Geranyl Diphosphate Synthase cDNAs. One full-length, in-frame clone from each putative geranyl diphosphate synthase allele was transformed into *E. coli* XL1-Blue and was grown to OD₆₀₀=0.7, induced with 1 mM IPTG and allowed to express for 6 h at 20°C. The bacteria were harvested by centrifugation, resuspended in assay buffer, and disrupted by brief sonication. The extract was cleared of debris by centrifugation and the resulting supernatant assayed using ¹⁴C-IPP and DMAPP as cosubstrates as described in Example 1, except that 1 mM PMSF, 1 mM EDTA and 0.1% Triton X-100 were included in the incubation mixture. One of the clones, designated Mp13.18, was shown to have the highest level of expressed activity and the cDNA insert was sequenced completely on both strands (SEQ ID No:1).

Plants employ different codon usage than *E. coli* and the presence of arginine codons AGA and AGG can lead to mistranslation or truncation of eukaryotic proteins when heterologously expressed in *E. coli*. Since nine of the 14 arginines in the clone Mp13.18 sequence are coded for by these rare *E. coli* tRNAs, the pET3a-derived vector, pSBETa, was chosen for expression. This vector, in addition to driving expression with T7 DNA polymerase from the strong T7lac promoter, carries the sequence encoding the tRNA for rare arginine codon usage (Schenk et al., *BioTechniques* 19:196-200, 1995).

To clone the open reading frame of Mp13.18 directionally into pSBETa, an *Nde*I site (CAT ATG) was added at the starting methionine by site directed mutagenesis (QuickChange, Stratagene), and a convenient *Bam*HI site (8 bp downstream of the stop codon) was utilized. The vector and engineered derivative of Mp13.18, designated Mp13.18N, were double digested with *Bam*HI and *Nde*I, the fragments were gel purified and ligated overnight, and then transformed into *E. coli* XL1-Blue competent cells. The resulting plasmid, designated pSB13.18, was purified, sequenced to verify that no undesired changes occurred during mutagenesis, and transformed into the T7 expression strain, *E. coli* BL21(DE3)pLysS. Clone

pSB13.18 was used in all subsequent studies of geranyl diphosphate synthase expression in *E. coli*. Expression in *E. coli* was performed as described above.

Confirmation of the identity of the putative GPP synthase encoded by plasmid Mp13.18 using the GPP synthase peptide amino acid sequence information.

5 Functional expression of a putative geranyl diphosphate synthase gene in *E. coli* does not absolutely prove that the cloned cDNA encodes geranyl diphosphate synthase. Functional expression of GPP synthase is complicated by the fact that the host cells used in all expression systems (plant, microbial and animal) contain competing phosphatases that can hydrolyse both the substrates (dimethylallyl diphosphate and
10 isopentenyl diphosphate) and the product (geranyl diphosphate) of the reaction catalyzed by GPP synthase. Consequently, there exists the possibility of false negative results in cell-free extracts of the recombinant enzyme.

Additionally, functional expression is complicated by the fact that all host cells (plant, microbial and animal) contain endogenous FPP synthase. This enzyme
15 synthesizes GPP (C_{10}) on route to the C_{15} homolog farnesyl diphosphate (see FIGURE 1), and it is known in the art that mutated, altered or otherwise degraded forms of FPP synthase (generated for example by cell breakage in the process of cell-free assay of the recombinant enzyme) will release the geranyl diphosphate intermediate, thus leading to a false positive indication of the presence of
20 GPP synthase (Wise, M.L. and Croteau, R., in Cane, D.E., ed., "Comprehensive Natural Products Chemistry: Isoprenoids, Vol. 2" Elsevier Science, Oxford, 1997 (in press); Ogura, K. and Koyama, T., in Ogura, K. and Sankawa, U., eds., "Dynamic Aspects of Natural Products Chemistry" Kodansha/Harwood Academic Publishers, Tokyo, pp. 1-23, 1997). Such artefactual formation of GPP is observed in *E. coli*
25 extracts and so extreme care and reproducibility, and the use of controls in each case, are required in monitoring recombinant enzyme activity.

Finally, one of the substrates of the reaction (dimethylallyl diphosphate) can displace the bound geranyl diphosphate intermediate of the FPP synthase enzyme, and so even minor alterations in the assay or reaction medium can give rise to false
30 positive indications for the presence of GPP synthase. The assay described herein was designed to minimize this complication, but this kinetic effect is highly variable and dependent on conditions of the medium. Thus, there are severe complications with functional heterologous expression of GPP synthase, primarily leading to false positives, that prevent reliance on functional expression as a means of confirming
35 clone identity. For this reason, and in spite of positive indication by functional

expression, the GPP synthase clone could be unambiguously confirmed only by matching the limited available GPP synthase amino acid sequence data from the purified protein to the amino acid sequence data derived from the putative geranyl diphosphate synthase cDNA.

- 5 Alignment of the two peptide sequences derived from purified GPP synthase (SEQ ID No:3 and SEQ ID No:7) with the deduced amino acid sequence of putative GPP synthase clone Mp 13.18 (SEQ ID No:2) revealed that the nine amino acid peptide (SEQ. ID No: 3) exactly corresponded to amino acid residues 254 to 262 of the putative GPP synthase sequence (SEQ ID No:2), while the eight amino acid
10 peptide (SEQ ID No:7) exactly corresponded to amino acid residues 184 to 191 of the putative GPP synthase sequence (SEQ ID No:2).

Example 3

Sequence Analysis of Geranyl Diphosphate Synthase cDNA Insert of Plasmid

Mp13.18

- 15 The geranyl diphosphate synthase clone encoded by the cDNA insert of Mp13.18 (1131 nt), which yielded the highest expressed level of synthase activity, contained an open reading frame of 939 nucleotides, corresponding to a protein of 313 amino acids with a calculated molecular weight of 33,465. The first 48 deduced amino acid residues show the expected characteristics of a plastidial targeting
20 sequence, *i.e.*, the sequence is rich in serine residues and amino acid residues with small, hydrophobic side chains, and is low in acidic residues (von Heijne et al., *Eur. J. Biochem.* 180:535-545, 1989). The presence of a putative, amino-terminal targeting sequence is consistent with the plastidial origin of monoterpene biosynthesis in plant cells (Wise, M.L. and Croteau, R., in Cane, D.E., ed., "Comprehensive Natural
25 Products Chemistry: Isoprenoids, Vol. 2" Elsevier Science, Oxford, 1997 (in press). By excluding the putative transit peptide residues, the amino acid sequence corresponds to a mature, processed protein of molecular weight 28,485, in full agreement with a molecular weight of about 29,000 (monomeric subunit size) determined for the native enzyme by SDS-PAGE.

- 30 An alignment of translated, plant-derived prenyltransferase sequences reveals a closer relationship between the *Mentha* geranyl diphosphate synthase and plant geranylgeranyl diphosphate synthases (~28% identity; ~54% similarity), than between the *Mentha* geranyl diphosphate synthase and plant farnesyl diphosphate synthases (~16% identity; ~40% similarity). The observation that the *Mentha* geranyl

diphosphate synthase is more closely related to geranylgeranyl diphosphate synthases than to farnesyl diphosphate synthases is consistent with the plastidial location of geranyl diphosphate synthase and geranylgeranyl diphosphate synthases, unlike farnesyl diphosphate synthases which are located in the cytoplasm. Although the

5 *Mentha* geranyl diphosphate synthase is more closely related to geranylgeranyl diphosphate synthases than to farnesyl diphosphate synthases, it is nonetheless apparent that there is low overall identity and similarity between the *Mentha* geranyl diphosphate synthase and either geranylgeranyl diphosphate synthases or farnesyl diphosphate synthases.

10 Comparison of percent identities at the nucleotide level reveals that the highest level of identity between the *Mentha* GPP synthase cDNA and a farnesyl diphosphate synthase cDNA clone is a value of 38% percent identity between the cDNA insert of plasmid Mp 13.18 and a farnesyl diphosphate synthase cDNA from *Zea mays* (Accession Number L39789). Similarly, the highest level of identity between the

15 *Mentha* GPP synthase cDNA and a geranylgeranyl diphosphate synthase cDNA is 44% percent identity between the cDNA insert of Mp 13.18 and a geranylgeranyl diphosphate synthase cDNA from *Arabidopsis thaliana* (Accession Number L25813). By comparison, completely unrelated nucleic acid sequences will yield a percent identity score of approximately 25%. Thus, the nucleotide sequence of the cDNA

20 insert of Mp13.18 is only distantly related to the nucleotide sequences of cDNAs encoding geranylgeranyl diphosphate synthase and farnesyl diphosphate synthase.

Example 4

Northern Analysis Demonstrating Hybridization of Peppermint GPP Synthase cDNA (SEQ ID No:1) to GPP Synthase Messenger RNA Molecules from Other Plant Species

25

Northern blot analysis was utilized to demonstrate hybridization between the peppermint GPP synthase cDNA set forth in SEQ ID No:1 and mRNA molecules encoding GPP synthase from other plant species. RNA was extracted from *Mentha spicata*, *Mentha candicans*, *Salvia officinalis* and *Perilla frutescens* and aliquots of

30 RNA from each of these species were separated on a denaturing agarose gel and blotted onto nylon membrane. The membrane was probed with radiolabelled peppermint GPP synthase cDNA (SEQ ID No:1) utilizing the following hybridization and wash conditions: hybridization in 3 X SSC at 65°C for 16 hours, followed by washing under the following conditions: two washes in 2 X SSC at 18°C to 25°C for

35 twenty minutes per wash, followed by two washes in 0.5 X SSC at 55°C for thirty

minutes per wash. Radiolabelled peppermint GPP synthase cDNA (SEQ ID No:1) remained hybridized, under the foregoing wash conditions, to homologous GPP synthase mRNAs from each of the plant species tested.

Example 5

5 Partial Length GPP Synthase cDNA Molecules Cloned from *Perilla frutescens* and *Salvia officinalis*

Partial-length cDNA fragments encoding a portion of a GPP synthase protein were amplified from mRNA extracted from *Perilla frutescens* and *Salvia officinalis*. A degenerate, forward PCR primer (SEQ ID No:8) was synthesized that
10 corresponded to the portion of the nucleic acid sequence set forth in SEQ ID No:1 that encodes amino acids 76-82 of the geranyl diphosphate synthase protein set forth in SEQ ID No:2. A degenerate, reverse PCR primer (SEQ ID No:9) was synthesized that corresponded to the portion of the nucleic acid sequence set forth in SEQ ID No:1 that encodes amino acids 124-129 of the geranyl diphosphate synthase protein
15 set forth in SEQ ID No:2. PCR amplification was carried out under the following conditions: 1 X PCR buffer containing 20 mM Tris-HCL (pH8.4), 50 mM KCl, 5mM MgCl₂, 0.5 mM of each dNTP, 2.5 units of Taq DNA polymerase, 50 pmol of the primer set forth in SEQ ID No:8, 50 pmol of the primer set forth in SEQ ID No:9 and 1 X 10⁶ lambda ZAPII cDNA library phage as template. The following temperature
20 cycling conditions were utilized: 2 minutes at 94°C followed by 30 cycles each of 1 minute at 94°C, followed by 30 seconds at 45°C and then 30 seconds at 72°C. PCR products were cloned using TOPO-TA according to the manufacturer's (Invitrogen) instructions.

Utilizing the foregoing PCR amplification conditions, a 161 bp cDNA
25 fragment was amplified and purified from *Perilla frutescens* (SEQ ID No:10). This fragment (SEQ ID No:10) corresponds to nucleotides 231 to 392 of the peppermint geranyl diphosphate synthase cDNA sequence set forth in SEQ ID No:1. Comparison of the partial-length *Perilla* GPP synthase cDNA sequence (SEQ ID No:10) with the corresponding region of the mint geranyl diphosphate synthase cDNA sequence set
30 forth in SEQ ID No:1 reveals 80% identity between the two, compared nucleic acid sequences. Comparison of the GPP synthase protein fragment (SEQ ID No:11), encoded by the *Perilla* GPP synthase partial-length cDNA sequence (SEQ ID No:10), with the corresponding region of the mint GPP synthase protein (amino acid residues 76 to 129 of the GPP synthase amino acid sequence set forth in SEQ ID No:2)
35 revealed 90% similarity between the two, compared amino acid sequences.

Similarly, utilizing the foregoing PCR amplification conditions, a 161 bp cDNA fragment was amplified and purified from *Salvia officinalis* (SEQ ID No:12). This fragment (SEQ ID No:12) corresponds to nucleotides 231 to 392 of the mint geranyl diphosphate synthase cDNA sequence set forth in SEQ ID No:1. Comparison
5 of the partial-length *Salvia officinalis* GPP synthase cDNA sequence (SEQ ID No:12) with the corresponding region of the mint geranyl diphosphate synthase cDNA sequence set forth in SEQ ID No:1 reveals 77% identity between the two, compared nucleic acid sequences. Comparison of the GPP synthase protein fragment (SEQ ID No:13), encoded by the *Salvia* GPP synthase partial-length cDNA sequence
10 (SEQ ID No:12), with the corresponding region of the mint GPP synthase protein (amino acid residues 76 to 129 of the GPP synthase amino acid sequence set forth in SEQ ID No:2) revealed 83% similarity between the two, compared amino acid sequences.

Example 6

15 Additional Representative Nucleic Acid Sequences Encoding Mint GPP Synthase

As set forth more fully in Example 2, *supra*, the PCR primers set forth in SEQ ID No:4 and SEQ ID No:5 were used to amplify a 113 bp cDNA fragment (SEQ ID No:6) which was used as a probe to isolate twenty seven homologous clones from a
20 *Mentha piperita* glandular trichome, secretory cell cDNA library. Sequencing revealed that the twenty seven clones represented three alleles. The biological activity of one clone from each of the three allele groups was tested by measuring geranyl diphosphate activity in supernatant derived from *E. coli* individually expressing each of the three, representative cDNAs. The clone showing the highest level of geranyl
25 diphosphate synthase activity was designated Mp13.18. The nucleotide sequence of Mp13.18 is set forth in SEQ ID No:1.

Additionally, the representative cDNA from each of the other two GPP synthase allelic groups was sequenced. The nucleic acid sequence of one GPP synthase allele, designated clone 13.11, is set forth in SEQ ID No:14, and the GPP
30 synthase protein encoded by the nucleic acid sequence set forth in SEQ ID No:14 is disclosed in SEQ ID No:15. The sequence of the other GPP synthase allele, designated clone 13.25, is set forth in SEQ ID No:16, and the GPP synthase protein encoded by the nucleic acid sequence set forth in SEQ ID No:16 is disclosed in SEQ ID No:17.

In addition to the nucleic acid sequence set forth in SEQ ID No:1, SEQ ID No:14 and SEQ ID No:16, examples of representative nucleic acid sequences of the present invention that encode a peppermint geranyl diphosphate synthase protein are set forth in SEQ ID No:18; SEQ ID No:19; SEQ ID No:20; SEQ ID No:21 and SEQ ID No:22. The nucleic acid sequences set forth in SEQ ID No:18; SEQ ID No:19; SEQ ID No:20; SEQ ID No:21 and SEQ ID No:22 were generated using a computer. By utilizing the degeneracy of the genetic code, the nucleic acid sequences set forth in SEQ ID No:18; SEQ ID No:19; SEQ ID No:20; SEQ ID No:21 and SEQ ID No:22 each has a different sequence, but each encodes the protein set forth in SEQ ID NO:2. Thus, the open reading frame of each of the nucleic acid molecules set forth in SEQ ID No:18; SEQ ID No:19; SEQ ID No:20; SEQ ID No:21 and SEQ ID No:22 extends from nucleotide 1 to nucleotide 939.

In addition to the protein sequences set forth in SEQ ID NO:2, SEQ ID No:15 and SEQ ID No:17 examples of representative geranyl diphosphate synthase proteins of the present invention are set forth in SEQ ID NO:23; SEQ ID NO:24; SEQ ID NO:25; SEQ ID NO:26; SEQ ID NO:27. The amino acid sequences set forth in SEQ ID NO:23; SEQ ID NO:24; SEQ ID NO:25; SEQ ID NO:26 and SEQ ID NO:27 were generated using a computer by making conservative amino acid substitutions in the peppermint GPP synthase protein sequence set forth in SEQ ID No:2.

Example 7

Hybridization of Peppermint Geranyl Diphosphate Synthase cDNA

(SEQ ID NO:1) to Other Nucleic Acid Sequences of the Present Invention

The nucleic acid molecules of the present invention are capable of hybridizing to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary sequence of the nucleic acid sequence set forth in SEQ ID NO:1, under the following stringent hybridization conditions: incubation in 5 X SSC at 65°C for 16 hours, followed by washing under the following conditions: two washes in 2 X SSC at 18°C to 25°C for twenty minutes per wash; preferably, two washes in 2 X SSC at 18°C to 25°C for twenty minutes per wash, followed by one wash in 0.5 X SSC at 55°C for thirty minutes; most preferably, two washes in 2 X SSC at 18°C to 25°C for fifteen minutes per wash, followed by two washes in 0.2 X SSC at 65°C for twenty minutes per wash.

The ability of the nucleic acid molecules of the present invention to hybridize to the nucleic acid sequence set forth in SEQ ID NO:1, or to the complementary

sequence of the nucleic acid sequence set forth in SEQ ID NO:1, can be determined utilizing the technique of hybridizing radiolabelled nucleic acid probes to nucleic acids immobilized on nitrocellulose filters or nylon membranes as set forth, for example, at pages 9.52 to 9.55 of Molecular Cloning, A Laboratory Manual (2nd edition), J. Sambrook, E.F. Fritsch and T. Maniatis eds, the cited pages of which are incorporated herein by reference.

Example 8

Properties of GPP Synthase Proteins of the Present Invention

Representative geranyl diphosphate synthase proteins of the present invention preferably possess the properties set forth in Table 3.

Table 3

Properties of Geranyl Diphosphate Synthase Proteins of the Present Invention

Cofactor requirement:	Divalent metal ion (usually Mg^{++} or Mn^{++} , potentially Fe^{++} , Co^{++} , Zn^{++})
pH optimum:	from about pH 6.2 to about pH 7.8
pI:	acidic, from about pH 4.5 to about pH 6.0
K_m (isopentenyl diphosphate):	<20 μM
K_m (dimethylallyl diphosphate):	<50 μM
K_m (metal ion):	Mg^{++} <5 mM; Mn^{++} <1 mM
k_{cat} :	<5/sec
Architecture:	Monomers or homodimers, with monomer molecular weight from about 30 kD to about 50 kD
Other properties:	Most are plastid-directed, operationally soluble, but relatively unstable enzymes. Highly specific for dimethylallyl diphosphate as allylic cosubstrate and for geranyl diphosphate as product (do not elongate beyond C_{10}). Inhibited by histidine- and arginine-directed reagents.

The embodiments of the invention in which an exclusive property or privilege is claimed are defined as follows:

1. An isolated nucleotide sequence encoding at least a portion of a geranyl diphosphate synthase protein.
2. An isolated nucleotide sequence of Claim 1 encoding at least a portion of an angiosperm geranyl diphosphate synthase protein.
3. An isolated nucleotide sequence of Claim 1 encoding at least a portion of a gymnosperm geranyl diphosphate synthase protein.
4. An isolated nucleotide sequence of Claim 1 encoding at least a portion of an essential oil plant geranyl diphosphate synthase protein.
5. An isolated nucleotide sequence of Claim 1 encoding at least a portion of a geranyl diphosphate synthase protein that occurs naturally in a member of the family Lamiaceae.
6. An isolated nucleotide sequence of Claim 1 encoding at least a portion of a *Mentha* geranyl diphosphate synthase protein.
7. An isolated nucleotide sequence of Claim 6 encoding at least a portion of a *Mentha piperita* geranyl diphosphate synthase protein.
8. An isolated nucleotide sequence of Claim 7 having the nucleotide sequence set forth in any one of SEQ ID No:1, SEQ ID No:14 and SEQ ID No:16.
9. An isolated nucleotide sequence of Claim 1 encoding at least a portion of a *Salvia* geranyl diphosphate synthase protein.
10. An isolated nucleotide sequence of Claim 9 encoding at least a portion of a *Salvia officinalis* geranyl diphosphate synthase protein.
11. An isolated nucleotide sequence of Claim 10 consisting of the nucleotide sequence set forth in SEQ ID No:12.
12. An isolated nucleotide sequence of Claim 1 encoding at least a portion of a *Perilla* geranyl diphosphate synthase protein.

13. An isolated nucleotide sequence of Claim 12 encoding at least a portion of a *Perilla frutescens* geranyl diphosphate synthase protein.

14. An isolated nucleotide sequence of Claim 13 consisting of the nucleotide sequence set forth in SEQ ID No:10.

15. An isolated, recombinant geranyl diphosphate synthase protein.

16. An isolated, recombinant, angiosperm geranyl diphosphate synthase protein of Claim 15.

17. An isolated, recombinant, gymnosperm geranyl diphosphate synthase protein of Claim 15.

18. An isolated, recombinant, essential oil plant geranyl diphosphate synthase protein of Claim 15.

19. An isolated, recombinant, geranyl diphosphate synthase protein of Claim 15, said protein occurring naturally in a member of the family Lamiaceae.

20. An isolated, recombinant, *Mentha* geranyl diphosphate synthase protein of Claim 15.

21. An isolated, recombinant, *Mentha piperita* geranyl diphosphate synthase protein of Claim 20.

22. An isolated, recombinant, *Mentha piperita* geranyl diphosphate synthase protein consisting of the amino acid sequence set forth in any one of SEQ ID No:2, SEQ ID No:15 and SEQ ID No:17.

23. A replicable expression vector comprising a nucleotide sequence of any one of Claims 1-14.

24. A replicable expression vector comprising a nucleotide sequence encoding a protein of any one of Claims 15-22.

25. A host cell comprising a vector of Claim 23 or Claim 24.

26. A method of imparting or enhancing the production of geranyl diphosphate synthase in a host cell comprising introducing into the host cell an expression vector of Claim 23 or Claim 24 under conditions enabling expression of the protein in the host cell.

27. The method of Claim 26 wherein the host cell is a eukaryotic cell.

28. The method of Claim 27 wherein the host cell is a plant cell.

29. The method of Claim 27 wherein the host cell is an animal cell.

30. A method of imparting or enhancing the production of geranyl diphosphate synthase in a host cell comprising introducing into the host cell an isolated, recombinant protein of any one of Claim 15, Claim 16, Claim 17, Claim 18, Claim 19, Claim 20, Claim 21 and Claim 22.

31. A method of treating cancer in a mammalian host comprising introducing into a cancerous cell a geranyl diphosphate synthase protein and a monoterpene synthase protein, said monoterpene synthase protein being capable of converting geranyl diphosphate to a monoterpene having anti-cancer properties.

32. The method of Claim 31 wherein said geranyl diphosphate synthase protein is from an essential oil plant species and said monoterpene synthase is limonene synthase.

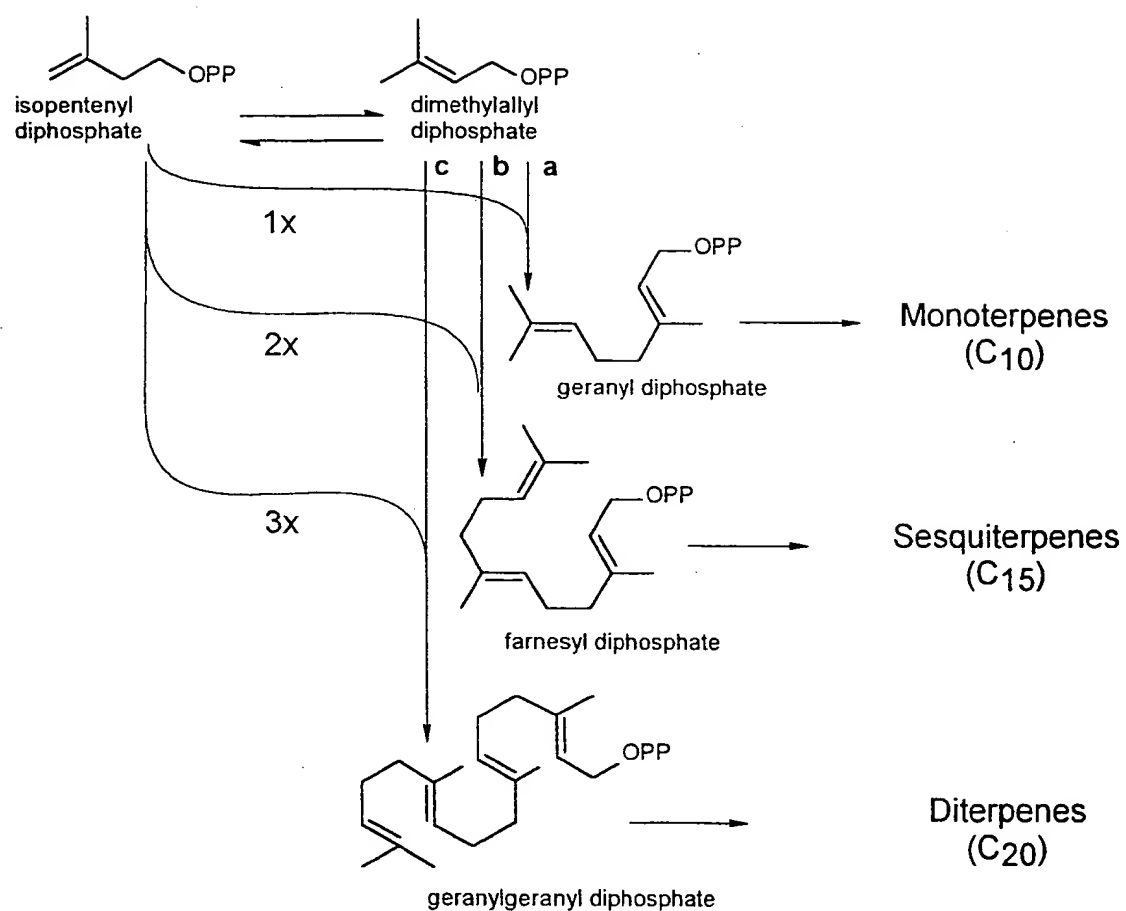
33. The method of Claim 31 wherein said geranyl diphosphate synthase protein is from a *Mentha* species and said monoterpene synthase is limonene synthase.

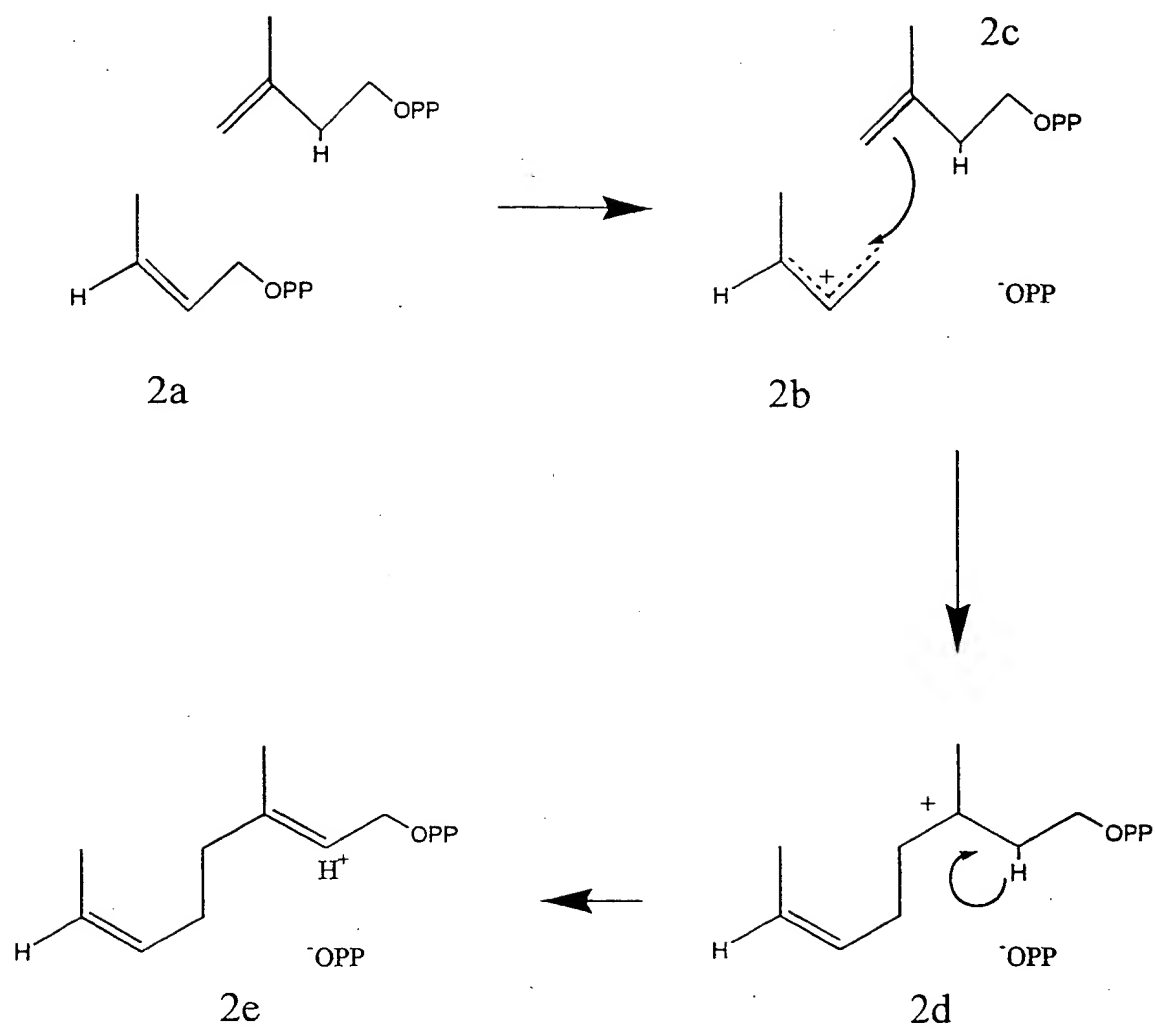
34. A method of treating cancer in a mammalian host comprising introducing into a cancerous cell both a nucleotide sequence encoding a geranyl diphosphate synthase protein and a nucleotide sequence encoding a monoterpene synthase protein, said monoterpene synthase protein being capable of converting geranyl diphosphate to a monoterpene having anticancer properties.

35. The method of Claim 34 wherein said geranyl diphosphate synthase protein is from an essential oil plant species and said monoterpene synthase is limonene synthase.

36. The method of Claim 34 wherein said geranyl diphosphate synthase protein is from a *Mentha* species and said monoterpene synthase is limonene synthase.

37. An isolated nucleotide sequence that is capable of hybridizing to the nucleotide sequence set forth in SEQ ID NO:1, or to the antisense complement of the nucleotide sequence set forth in SEQ ID NO:1, under stringent conditions.

**Figure 1**

**Figure 2**

SEQUENCE LISTING

<110> Croteau, Rodney B
 Wildung, Mark R
 Burke, Charles C
 Gershenzon, Jonathan

<120> Geranyl Diphosphate Synthase from Mint (*Mentha piperita*)

<130> wsur12998

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<150> 08/951,924

<151> 1997-10-16

<160> 27

<170> PatentIn Ver. 2.0

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<222> (6)..(944)

<400> 1

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ctc aaa aca aga tct gat ctc agc cgt tct tct tcc gcg cgt tgc atg   98
Leu Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met
           20             25             30

cca act gcc gcc gct gcc gcc ttc ccc act atc gcc acc gcc gcc caa  146
Pro Thr Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln
           35             40             45

agt cag ccg tac tgg gcc gcc atc gag gcc gac ata gag aga tac ctg  194
Ser Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu
           50             55             60

```

aag aaa tcc atc aca ata agg ccg ccg gag aca gtt ttc ggg ccc atg	242
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His His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys	
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ttg gcg gcg tgc gag ctc gtc ggc ggc gac cga agc caa gcc atg gca	338
Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala	
100 105 110	
gcc gcg gcg gcg atc cat ctc gtg cac gcg gca gcc tac gtc cac gag	386
Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu	
115 120 125	
cac ctc cct cta acc gac ggg tgc agg ccc gta tcc aag ccc gca atc	434
His Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile	
130 135 140	
cag cac aag tac ggc ccg aac gtc gag ctc ctc acc gga gac ggg att	482
Gln His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile	
145 150 155	
gtc ccg ttc ggg ttt gag ttg ctg gcc ggg tca gtg gac ccg gcc cga	530
Val Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg	
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aca gac gac ccg gat agg att ctg aga gtt ata ata gag atc agt cgg	578
Thr Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg	
180 185 190	
gcc ggc ggg ccg gag gga atg ata agc ggg ctg cat agg gaa gaa gaa	626
Ala Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu	
195 200 205	
att gtt gat gga aat acg agt tta gac ttc att gaa tat gtg tgc aag	674
Ile Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys	
210 215 220	
aaa aaa tac ggc gag atg cat gct tgc ggc gcg gct tgt gga gcc ata	722
Lys Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile	
225 230 235	
ttg ggc ggc gca gcc gag gag gag att cag aag ctg agg aat ttc ggg	770
Leu Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly	
240 245 250 255	

ctt tat caa gga act ctc aga gga atg atg gaa atg aaa aat tct cat 818
 Leu Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His
 260 265 270

caa tta att gat gag aat ata att gga aaa ttg aaa gaa ttg gct ctc 866
 Gln Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu
 275 280 285

gag gag ttg gga ggc ttc cac ggg aag aac gct gag ctg atg tcg agc 914
 Glu Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser
 290 295 300

ctt gta gcc gag ccg agc ctt tac gcg gct tagagctatt cggatccttc 964
 Leu Val Ala Glu Pro Ser Leu Tyr Ala Ala
 305 310

attgcatttt catgcgacat cttcatattc atattgcata atatttttta agccagttat 1024
 ttttttatta tgaatttttt taactgttat tgatttcgaa aatactgaca atcatctaaa 1084
 ataaagtaaa tatagtaagg atgaaaaaaaa aaaaaaaaaa aaaaaaa 1131

<210> 2

<211> 313

<212> PRT

<213> Mentha piperita

<400> 2

Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro Leu
 1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
 20 25 30

Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
 35 40 45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
 50 55 60

Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
 85 90 95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala

100	105	110
Ala Ala Ala Ile His Leu Val	His Ala Ala Ala Tyr Val	His Glu His
115	120	125
Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser	Lys Pro Ala Ile Gln	
130	135	140
His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val		
145	150	155
		160
Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr		
165	170	175
Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala		
180	185	190
Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile		
195	200	205
Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys		
210	215	220
Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu		
225	230	235
		240
Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu		
245	250	255
Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln		
260	265	270
Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu		
275	280	285
Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu		
290	295	300
Val Ala Glu Pro Ser Leu Tyr Ala Ala		
305	310	

<210> 3
 <211> 9
 <212> PRT
 <213> *Mentha spicata*

<400> 3

Phe Gly Leu Tyr Gln Gly Thr Leu Arg
1 5

<210> 4

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> Oligonucleotide forward PCR primer for cloning GPP
synthase cDNAs from peppermint

<400> 4

ttccctctca aaacaagatc ag

22

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> Reverse oligonucleotide PCR primer for cloning GPP
synthase cDNAs from peppermint

<400> 5

tacggctgat tttgggcgg

19

<210> 6

<211> 113

<212> DNA

<213> Mentha piperita

<400> 6

ttccctctca aaacaagatc agatctcagc cgttctcctt cagcacgttg catgcccact 60
 gccgtcgctg ccgtcttgcc cactctcgcc accgccgcc aaaatcagcc gta 113

<210> 7
 <211> 8
 <212> PRT
 <213> *Mentha spicata*

<400> 7
 Arg Val Ile Ile Glu Ile Ser Arg
 1 5

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> Forward degenerate PCR primer used to clone GPP
 synthase cDNA homologs

<400> 8
 ttyggnccna tgca yca

17

<210> 9
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide primer

<220>
 <221> misc_feature
 <222> (1)..(17)
 <223> Reverse degenerate oligonucleotide PCR primer used
 to amplify GPP synthase cDNA homologs

<400> 9

arrtgytcrtnacarta

17

<210> 10

<211> 161

<212> DNA

<213> *Perilla frutescens*

<220>

<221> CDS

<222> (1)..(159)

<400> 10

ttt gga cca atg cac cat ctc acc ttt gcg gcc cca ggg acc gca gcc	48
Phe Gly Pro Met His His Leu Thr Phe Ala Ala Pro Gly Thr Ala Ala	
1 5 10 15	

aac acc ctc tgc ctg gcg gca tgc gag ctc gtg ggc ggg gag aaa agc	96
Asn Thr Leu Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Glu Lys Ser	
20 25 30	

cag gcg atg cca tcc gcg gcg gcc atc cac atc gtc cac gca gga gcc	144
Gln Ala Met Pro Ser Ala Ala Ala Ile His Ile Val His Ala Gly Ala	
35 40 45	

tat gta cac gaa cac ct	161
Tyr Val His Glu His	
50	

<210> 11

<211> 53

<212> PRT

<213> *Perilla frutescens*

<400> 11

Phe Gly Pro Met His His Leu Thr Phe Ala Ala Pro Gly Thr Ala Ala
1 5 10 15

Asn Thr Leu Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Glu Lys Ser
20 25 30

Gln Ala Met Pro Ser Ala Ala Ala Ile His Ile Val His Ala Gly Ala
35 40 45

Tyr Val His Glu His

50

<210> 12
 <211> 161
 <212> DNA
 <213> *Salvia officinalis*

<220>
 <221> CDS
 <222> (1)..(159)

<400> 12
 ttc ggc cct atg cat cat ctc ctc ttc gcg ggc ccc ggc acc ggc gcc 48
 Phe Gly Pro Met His His Leu Leu Phe Ala Gly Pro Gly Thr Gly Ala
 1 5 10 15

 tct atg tta tgc ctc gcg gcc tgc gag ctc gtg ggc ggg gag cgg agc 96
 Ser Met Leu Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Glu Arg Ser
 20 25 30

 cag ggc atg gcc tcc ggg gcg gcg ctc cac cta gtc cat gcg gga gcc 144
 Gln Gly Met Ala Ser Gly Ala Ala Leu His Leu Val His Ala Gly Ala
 35 40 45

 tac gtg cac gaa cat tt 161
 Tyr Val His Glu His
 50

<210> 13
 <211> 53
 <212> PRT
 <213> *Salvia officinalis*

<400> 13
 Phe Gly Pro Met His His Leu Leu Phe Ala Gly Pro Gly Thr Gly Ala
 1 5 10 15

 Ser Met Leu Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Glu Arg Ser
 20 25 30

 Gln Gly Met Ala Ser Gly Ala Ala Leu His Leu Val His Ala Gly Ala
 35 40 45

 Tyr Val His Glu His
 50

<210> 14
 <211> 936
 <212> DNA
 <213> *Mentha piperita*

<220>
 <221> CDS
 <222> (1)..(933)

<400> 14
 atg gcc att aat ctt tcc cat atc aac tcc aaa acg agt ttc cct ctc 48
 Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Ser Phe Pro Leu
 1 5 10 15
 aaa aca aga tct gat ctg agc cgt tct tct tca gcg cgt tgc atg cca 96
 Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
 20 25 30
 act gcc gcc gct gcc gtc ttc ccc act atc gcc acc gcc gcc caa agt 144
 Thr Ala Ala Ala Ala Val Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
 35 40 45
 cag ccg tat tgg gcc gcc atc gtg gcc gac ata gac aga tac ctg aag 192
 Gln Pro Tyr Trp Ala Ala Ile Val Ala Asp Ile Asp Arg Tyr Leu Lys
 50 55 60
 aaa tcc atc cca ata agg ccg ccg gag act gtt ttc ggg ccc atg cac 240
 Lys Ser Ile Pro Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80
 cac ctc acc ttc gcc gct cca gcc acc gcc gcc tcc gcc tcc gcc ctg 288
 His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Ala Ser Ala Leu
 85 90 95
 tgt ttg gcg gcg tgc gag ctc gtc ggc gga gac cga agc caa gcc atg 336
 Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met
 100 105 110
 gct gcc gcc gcg gcg att cat ctc atg cac gcg gca gcc tac gtc cac 384
 Ala Ala Ala Ala Ala Ile His Leu Met His Ala Ala Ala Tyr Val His
 115 120 125
 gag cac ctc cct cta acc gac ggg tcg agg aag ccc gca atc cag cac 432
 Glu His Leu Pro Leu Thr Asp Gly Ser Arg Lys Pro Ala Ile Gln His
 130 135 140
 aag tac ggc ccg aac gtc gag ctc ctc acc gga gat ggg att gtt ccg 480

Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val Pro
 145 150 155 160
 ttc ggg ttt gag ttg ctg gcc ggg tct gtg gac ccg gcc cga aga gac 528
 Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Arg Asp
 165 170 175
 gac ccg gat aga att ctg agg gtt ata ata gag atc agt ccg gcc ggc 576
 Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala Gly
 180 185 190
 ggg tcg gag gga ata ata agc ggg ctg cat agg gaa gaa gaa att gtt 624
 Gly Ser Glu Gly Ile Ile Ser Gly Leu His Arg Glu Glu Glu Ile Val
 195 200 205
 gat gga aat acg agt ttc gac ttc att gaa tat gtg tgt aag aaa aaa 672
 Asp Gly Asn Thr Ser Phe Asp Phe Ile Glu Tyr Val Cys Lys Lys Lys
 210 215 220
 tac ggc gag atg cat gct tgc ggc gcg gct tgt gga gcc ata ttg ggc 720
 Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu Gly
 225 230 235 240
 ggc gca gcc gag gag gag att cag aag ctg agg aat ttc ggg ctt tat 768
 Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu Tyr
 245 250 255
 caa gga act ctc aga gga atg atg gaa atg aaa aat tct cat gaa att 816
 Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Glu Ile
 260 265 270
 gat gat aat ata att aga aaa ttg aaa gaa ttg gct ctc gag gag ttg 864
 Asp Asp Asn Ile Ile Arg Lys Leu Lys Glu Leu Ala Leu Glu Glu Leu
 275 280 285
 gga ggc ttc cac gga aag cag gct gag ctg atg tcc agc ctt gta gcc 912
 Gly Gly Phe His Gly Lys Gln Ala Glu Leu Met Ser Ser Leu Val Ala
 290 295 300
 ggg ccg agc cct tgt gcg gct tag 936
 Gly Pro Ser Pro Cys Ala Ala
 305 310

<210> 15

<211> 311

<212> PRT

<213> Mentha piperita

<400> 15

Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Ser Phe Pro Leu
1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
20 25 30

Thr Ala Ala Ala Ala Val Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
35 40 45

Gln Pro Tyr Trp Ala Ala Ile Val Ala Asp Ile Asp Arg Tyr Leu Lys
50 55 60

Lys Ser Ile Pro Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Ala Ser Ala Leu
85 90 95

Cys Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met
100 105 110

Ala Ala Ala Ala Ala Ile His Leu Met His Ala Ala Ala Tyr Val His
115 120 125

Glu His Leu Pro Leu Thr Asp Gly Ser Arg Lys Pro Ala Ile Gln His
130 135 140

Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val Pro
145 150 155 160

Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Arg Asp
165 170 175

Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala Gly
180 185 190

Gly Ser Glu Gly Ile Ile Ser Gly Leu His Arg Glu Glu Glu Ile Val
195 200 205

Asp Gly Asn Thr Ser Phe Asp Phe Ile Glu Tyr Val Cys Lys Lys Lys
210 215 220

Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu Gly
225 230 235 240

Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu Tyr

<210> 16
<211> 936
<212> DNA
<213> *Mentha piperita*

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<220>  
<221> CDS  
<222> (1)..(933)
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<400> 16																	
atg gcc att aat ctt tcc cat atc aac tcc aaa acc agt ttc cct ctc	48																
Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Ser Phe Pro Leu																	
1 5 10 15																	
aaa aca aga tca gat ctc agc cgt tct cct tca gca cgt tgc atg ccc	96																
Lys Thr Arg Ser Asp Leu Ser Arg Ser Pro Ser Ala Arg Cys Met Pro																	
20 25 30																	
act gcc gtc gct gcc gtc ttg ccc act ctc gcc acc gcc gcc caa aat	144																
Thr Ala Val Ala Ala Val Leu Pro Thr Leu Ala Thr Ala Ala Gln Asn																	
35 40 45																	
cag ccg tat tgg gcc gcc ata gag gcc gac ata gac aga tat ctg aag	192																
Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Asp Arg Tyr Leu Lys																	
50 55 60																	
aaa tcc atc cca ata agg ccg ccg gag act gta ttc ggg ccc atg cac	240																
Lys Ser Ile Pro Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His																	
65 70 75 80																	
cac ctc acc ttc gcc gcc cca gcc acc acc gcc tcc gcc cta tgc ttg	288																
His Leu Thr Phe Ala Ala Pro Ala Thr Thr Ala Ser Ala Leu Cys Leu																	
85 90 95																	

gcg gcg tgc gag ctc gtc ggc ggc gac cgg aac caa gcc atg gct gcc 336
 Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Asn Gln Ala Met Ala Ala
 100 105 110

gcc gcg gcg att cat ctc atg cac gcg gca gcc tac gcc cac gag cac 384
 Ala Ala Ala Ile His Leu Met His Ala Ala Ala Tyr Ala His Glu His
 115 120 125

ctc cct cta acc gat ggg tcg agg ccc gaa tcc aag ccc gca atc cag 432
 Leu Pro Leu Thr Asp Gly Ser Arg Pro Glu Ser Lys Pro Ala Ile Gln
 130 135 140

cac aag tac ggc ccg aac gtc gag ctc ctc acc gga gat ggg atc gct 480
 His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Ala
 145 150 155 160

ccg ttc ggg ttc gag ttg ctg gcc ggg tct gtt gac ccg gcc cga aga 528
 Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Arg
 165 170 175

gac gac ccg gat aga atc ctg aga gtt gta ata gag atc agt cgg gcc 576
 Asp Asp Pro Asp Arg Ile Leu Arg Val Val Ile Glu Ile Ser Arg Ala
 180 185 190

agc ggg tcg gag gga atg gta agc ggg ctg tat agg gaa gcg gaa att 624
 Ser Gly Ser Glu Gly Met Val Ser Gly Leu Tyr Arg Glu Ala Glu Ile
 195 200 205

gtt gat gaa gat acg agg tta gag ttc att gaa tat gtg tgt aag aaa 672
 Val Asp Glu Asp Thr Arg Leu Glu Phe Ile Glu Tyr Val Cys Lys Lys
 210 215 220

aaa tac ggc gag atg cat gct tgc ggc gcg gct tgt gga gcc ata ttg 720
 Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu
 225 230 235 240

ggc ggc ggc gcc gaa gag gag att cag aag ctg agg aat ttc ggg ctt 768
 Gly Gly Gly Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu
 245 250 255

tat gta gga act ctt aga gga atg ctg gaa aag aaa aat tct cat gaa 816
 Tyr Val Gly Thr Leu Arg Gly Met Leu Glu Lys Lys Asn Ser His Glu
 260 265 270

att gag aaa ata att aga aaa ttg aaa gaa ttg gct ctc gag gag ttg 864
 Ile Glu Lys Ile Ile Arg Lys Leu Lys Glu Leu Ala Leu Glu Glu Leu
 275 280 285

gaa ggc ttc cac gga aag aac gtt gag ctg atg tcg agc ctt gta gct 912
 Glu Gly Phe His Gly Lys Asn Val Glu Leu Met Ser Ser Leu Val Ala
 290 295 300

gag ccg acc ctt agc gca gct tag 936
 Glu Pro Thr Leu Ser Ala Ala
 305 310

<210> 17
 <211> 311
 <212> PRT
 <213> *Mentha piperita*

<400> 17
 Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Ser Phe Pro Leu
 1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Pro Ser Ala Arg Cys Met Pro
 20 25 30

Thr Ala Val Ala Ala Val Leu Pro Thr Leu Ala Thr Ala Ala Gln Asn
 35 40 45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Asp Arg Tyr Leu Lys
 50 55 60

Lys Ser Ile Pro Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Thr Ala Ser Ala Leu Cys Leu
 85 90 95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Asn Gln Ala Met Ala Ala
 100 105 110

Ala Ala Ala Ile His Leu Met His Ala Ala Ala Tyr Ala His Glu His
 115 120 125

Leu Pro Leu Thr Asp Gly Ser Arg Pro Glu Ser Lys Pro Ala Ile Gln
 130 135 140

His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Ala
 145 150 155 160

Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Arg
 165 170 175

Asp Asp Pro Asp Arg Ile Leu Arg Val Val Ile Glu Ile Ser Arg Ala
 180 185 190
 Ser Gly Ser Glu Gly Met Val Ser Gly Leu Tyr Arg Glu Ala Glu Ile
 195 200 205
 Val Asp Glu Asp Thr Arg Leu Glu Phe Ile Glu Tyr Val Cys Lys Lys
 210 215 220
 Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu
 225 230 235 240
 Gly Gly Gly Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu
 245 250 255
 Tyr Val Gly Thr Leu Arg Gly Met Leu Glu Lys Lys Asn Ser His Glu
 260 265 270
 Ile Glu Lys Ile Ile Arg Lys Leu Lys Glu Leu Ala Leu Glu Glu Leu
 275 280 285
 Glu Gly Phe His Gly Lys Asn Val Glu Leu Met Ser Ser Leu Val Ala
 290 295 300
 Glu Pro Thr Leu Ser Ala Ala
 305 310

<210> 18
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence encoding peppermint GPP synthase

<220>
 <221> misc_difference
 <222> (1)..(942)
 <223> Computer-generated nucleic acid sequence encoding
 peppermint GPP synthase

<400> 18
 atggccatta acctctccca tatcaactcc aaaacatgtt tccctctcaa aacaagatct 60
 gatctcagcc gttcttcttc cgcgcgttgc atgccaaactg ccgcccgtgc cgccttcccc 120

actatcgcca cgcgcgcca aagtcagccg tactgggccc ccatcgaggc cgacatagag 180
 agatacctga agaaatccat cacaataagg ccgccggaga cagttttcgg gcccatgcac 240
 cacctcacct tcgcccggcc agccaccgcc gcctccaccc tatgcttggc ggcgtgcgag 300
 ctgctcggcg gcgaccgaag ccaagccatg gcagccgcgg cggcgatcca tctcgtgcac 360
 gcggcagcct acgtccacga gcacctccct ctaaccgacg ggtcgaggcc cgtatccaag 420
 cccgcaatcc agcacaagta cggcccgaac gtcgagctcc tcaccggaga cgggattgtc 480
 ccgttcgggt ttgagttgct ggccgggtca gtggaccggy cccgaacaga cgaccgggat 540
 aggattctga gagttataat agagatcagt cgggccggcg ggccggaggg aatgataagc 600
 gggctgcata gggaagaaga aattgttgat ggaaatacga gtttagactt cattgaatat 660
 gtgtgcaaga aaaaatacgg cgagatgcat gcttgccggc cggcttctgg agccatattg 720
 ggccgcgag ccgaggagga gattcagaag ctgaggaatt tcgggcttta tcaaggaact 780
 ctcagaggaa tgatggaaat gaaaaattct catcaattaa ttgatgagaa tataattgga 840
 aaattgaaag aattggctct cgaggagttg ggaggcttcc acgggaagaa cgctgagctg 900
 atgtcgagcc ttgtagccga gccgagcctt tacgcggctt ag 942

<210> 19

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding peppermint GPP synthase protein

<220>

<221> misc_difference

<222> (1)..(942)

<223> Computer-generated nucleic acid sequence encoding
peppermint GPP synthase protein set forth in SEQ
ID NO:2

<400> 19

atggccatta atctctccca catcaactcc aaaacatgtt tccctctcaa aacaagatct 60

gatctcagcc gttcttcttc cgcgcgttgc atgccaactg ccgccgctgc cgccttcccc 120
actatcgcca ccgccgcca aagtcagccg tactgggccc ccatcgaggc cgacatagag 180
agatacctga agaaatccat cacaataagg ccgccggaga cagttttcgg gcccatgcac 240
cacctcacct tcgccgcccc agccaccgcc gcctccaccc tatgcttggc ggcgtgcgag 300
ctcgtcggcg gcgaccgaag ccaagccatg gcagccgcgg cggcgatcca tctcgtgcac 360
gcggcagcct acgtccacga gcacctccct ctaaccgacg ggtcgaggcc cgtatccaag 420
cccgcaatcc agcacaagta cggcccgaac gtcgagctcc tcaccggaga cgggattgtc 480
ccgttcgggt ttgagttgct ggccgggtca gtggaccggg cccgaacaga cgaccggat 540
aggattctga gagttataat agagatcagt cgggccggcg ggccggaggg aatgataagc 600
gggctgcata gggaagaaga aattgttgat ggaaatacga gtttagactt cattgaatat 660
gtgtgcaaga aaaaatacgg cgagatgcat gcttgccggc cggcttgtgg agccatattg 720
ggcggcgag cagaggagga gattcagaag ctgaggaatt tcgggcttta tcaaggaact 780
ctcagaggaa tgatggaaat gaaaaattct catcaattaa ttgatgagaa tataattgga 840
aaattgaaag aattggctct cgaggagtgt ggaggcttcc acgggaagaa cgctgagctg 900
atgtcgagcc ttgtagccga gccgagcctt tacgggctt ag 942

<210> 20

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding peppermint GPP synthase

<220>

<221> misc_difference

<222> (1)..(942)

<223> Computer-generated nucleic acid sequence encoding
peppermint GPP synthase sequence set forth in SEQ
ID NO:2

<400> 20
 atggccatta atctctccca tatcaactct aaaacatgtt tccctctcaa aacaagatct 60
 gatctcagcc gttcttcttc cgcgcggtgc atgccaaactg ccgcccgtgc cgccttcccc 120
 actatcgcca ccgcccacca aagtcagccg tactgggccc ccatcgaggc cgacatagag 180
 agatacctga agaaatccat cacaataagg ccgcccggaga cagttttcgg gcccatgcac 240
 cacctcacct tcgcccggcc agccaccgcc gcctccaccc tatgcttggc ggcgtgcgag 300
 ctgctcggcg gcgaccgaag ccaagccatg gcagccgagg cggcgatcca tctcgtgcac 360
 gcggcagcct acgtccacga gcacctccct ctaaccgacg ggtcgaggcc cgtatccaag 420
 cccgcaatcc agcacaagta cggcccgaac gtcgagctcc tcaccggaga cgggattgtc 480
 ccgttcgggt ttgagttgct ggccgggtca gtggaccggg cccgaacaga cgaccgggat 540
 aggattctga gagttataat agagatcagt cgggccggcg ggccggaggg aatgataagc 600
 gggctgcata gggaagaaga aattgttgat ggaaatacga gtttagactt cattgaatat 660
 gtgtgcaaga aaaaatacgg cgagatgcat gcttgccggc cggtttgtgg agccatattg 720
 ggcggcgag ccgaggagga gattcagaag ctgaggaatt tcgggcttta tcaaggaact 780
 ctgagaggaa tgatggaaat gaaaaattct catcaattaa ttgatgagaa tataattgga 840
 aaattgaaag aattggctct cgaggagttg ggaggcttcc acgggaagaa cgctgagctg 900
 atgtcgagcc ttgtagccga gccgagcctt tacgggctt ag 942

<210> 21
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence encoding peppermint GPP synthase
 <220>
 <221> misc_difference
 <222> (1)..(942)
 <223> Computer-generated nucleic acid sequence encoding
 peppermint GPP synthase protein sequence set forth

in SEQ ID NO:2

<400> 21

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atggccatta atctctccca tatcaactcc aaaacatgtt tccctcttaa aacaagatct 60
gatctcagcc gttcttcttc cgcgcgttgc atgccaactg ccgccgctgc cgccttcccc 120
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agatacctga agaaatccat cacaataagg ccgccggaga cagttttcgg gcccatgcac 240
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cccgcaatcc agcacaagta cggcccgaac gtcgagctcc tcaccggaga cgggattgtc 480
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gtgtgcaaga aaaaatacgg cgagatgcat gcttgccggc cggcttgtgg agccatattg 720
ggcggcgagc ccgaggagga gattcagaag ctgaggaatt tcgggcttta tcaaggaact 780
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942

<210> 22

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid
sequence encoding peppermint GPP synthase protein

<220>

<221> misc_difference

<222> (1)..(942)

<223> Computer-generated nucleic acid sequence encoding
peppermint GPP synthase protein sequence set forth
in SEQ ID NO:2

<400> 22

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actatcgcca ccgccgcccc aagtcagccg tactgggccg ccatcgaggc cgacatagag 180
agatacctga agaaatccat cacaataagg ccgccggaga cagttttcgg gcccatgcac 240
cacctcacct tcgccgcccc agccaccgcc gcctccaccc tatgcttggc ggcgtgcgag 300
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gcggcagcct acgtccacga gcacctccct ctaaccgacg ggtcgaggcc cgtatccaag 420
cccgcaatcc agcacaagta cggcccgaac gtcgagctcc tcaccggaga cgggattgtc 480
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<210> 23

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GPP synthase
protein variant

<220>

<221> VARIANT

<222> (1)..(313)

<223> Computer-generated peppermint GPP synthase protein
variant

<400> 23

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Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro Leu
  1             5             10             15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
          20             25             30

Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
      35             40             45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
      50             55             60

Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
      65             70             75             80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
          85             90             95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala
      100             105             110

Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His
      115             120             125

Leu Pro Leu Thr Asp Ala Ser Arg Pro Val Ser Lys Pro Ala Ile Gln
      130             135             140

His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val
      145             150             155             160

Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr
          165             170             175

Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala
      180             185             190

Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile
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Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys
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<400> 24
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Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
      20                      25                      30
Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
      35                      40                      45
Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
      50                      55                      60
Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His

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65		70		75		80
His Leu Thr Phe	Ala Ala Pro Ala Thr	Ala Ala Ser Thr	Leu Cys Leu			
	85		90		95	
Ala Ala Cys Glu	Leu Val Gly Gly	Asp Arg Ser Gln	Ala Met Ala Ala			
	100	105	110			
Ala Ala Ala Ile	His Leu Val His	Ala Ala Ala Tyr	Val His Glu His			
	115	120	125			
Leu Pro Leu Thr	Asp Gly Ser Lys	Pro Val Ser Lys	Pro Ala Ile Gln			
	130	135	140			
His Lys Tyr Gly	Pro Asn Val Glu	Leu Leu Thr Gly	Asp Gly Ile Val			
145	150	155	160			
Pro Phe Gly Phe	Glu Leu Leu Ala	Gly Ser Val Asp	Pro Ala Arg Thr			
	165	170	175			
Asp Asp Pro Asp	Arg Ile Leu Arg	Val Ile Ile Glu	Ile Ser Arg Ala			
	180	185	190			
Gly Gly Pro Glu	Gly Met Ile Ser	Gly Leu His Arg	Glu Glu Glu Ile			
	195	200	205			
Val Asp Gly Asn	Thr Ser Leu Asp	Phe Ile Glu Tyr	Val Cys Lys Lys			
210	215	220				
Lys Tyr Gly Glu	Met His Ala Cys	Gly Ala Ala Cys	Gly Ala Ile Leu			
225	230	235	240			
Gly Gly Ala Ala	Glu Glu Glu Ile	Gln Lys Leu Arg	Asn Phe Gly Leu			
	245	250	255			
Tyr Gln Gly Thr	Leu Arg Gly Met	Met Glu Met Lys	Asn Ser His Gln			
	260	265	270			
Leu Ile Asp Glu	Asn Ile Ile Gly	Lys Leu Lys Glu	Leu Ala Leu Glu			
	275	280	285			
Glu Leu Gly Gly	Phe His Gly Lys	Asn Ala Glu Leu	Met Ser Ser Leu			
290	295	300				
Val Ala Glu Pro	Ser Leu Tyr Ala	Ala Ala				
305	310					

<210> 25
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peppermint GPP
 synthase protein variant

<220>
 <221> VARIANT
 <222> (1)..(313)
 <223> Computer-generated peppermint GPP synthase protein
 variant

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 1 5 10 15
 Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
 20 25 30
 Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
 35 40 45
 Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
 50 55 60
 Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80
 His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
 85 90 95
 Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala
 100 105 110
 Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His
 115 120 125
 Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Ala Ala Ile Gln
 130 135 140
 His Lys Tyr Gly Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val
 145 150 155 160
 Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr
 165 170 175

Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala
 180 185 190
 Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile
 195 200 205
 Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys
 210 215 220
 Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu
 225 230 235 240
 Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu
 245 250 255
 Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln
 260 265 270
 Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu
 275 280 285
 Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu
 290 295 300
 Val Ala Glu Pro Ser Leu Tyr Ala Ala
 305 310

<210> 26

<211> 313

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peppermint GPP synthase protein variant

<220>

<221> VARIANT

<222> (1)..(313)

<223> Computer-generated peppermint GPP synthase protein variant

<400> 26

Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro Leu
 1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
 20 25 30
 Thr Ala Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
 35 40 45
 Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
 50 55 60
 Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80
 His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
 85 90 95
 Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala
 100 105 110
 Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His
 115 120 125
 Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile Gln
 130 135 140
 His Lys Tyr Ala Pro Asn Val Glu Leu Leu Thr Gly Asp Gly Ile Val
 145 150 155 160
 Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr
 165 170 175
 Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala
 180 185 190
 Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile
 195 200 205
 Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys
 210 215 220
 Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu
 225 230 235 240
 Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu
 245 250 255
 Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln
 260 265 270

Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu
 275 280 285

Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu
 290 295 300

Val Ala Glu Pro Ser Leu Tyr Ala Ala
 305 310

<210> 27

<211> 313

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: peppermint GPP
 synthase sequence variant

<220>

<221> VARIANT

<222> (1)..(313)

<223> Computer-generated peppermint GPP synthase protein
 variant

<400> 27

Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro Leu
 1 5 10 15

Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met Pro
 20 25 30

Thr Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln Ser
 35 40 45

Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu Lys
 50 55 60

Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met His
 65 70 75 80

His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys Leu
 85 90 95

Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala Ala
 100 105 110

Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu His

115	120	125
Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile Gln		
130	135	140
His Lys Tyr Gly Pro Asn Val Glu Ile Leu Thr Gly Asp Gly Ile Val		
145	150	155 160
Pro Phe Gly Phe Glu Leu Leu Ala Gly Ser Val Asp Pro Ala Arg Thr		
	165	170 175
Asp Asp Pro Asp Arg Ile Leu Arg Val Ile Ile Glu Ile Ser Arg Ala		
	180	185 190
Gly Gly Pro Glu Gly Met Ile Ser Gly Leu His Arg Glu Glu Glu Ile		
	195	200 205
Val Asp Gly Asn Thr Ser Leu Asp Phe Ile Glu Tyr Val Cys Lys Lys		
	210	215 220
Lys Tyr Gly Glu Met His Ala Cys Gly Ala Ala Cys Gly Ala Ile Leu		
225	230	235 240
Gly Gly Ala Ala Glu Glu Glu Ile Gln Lys Leu Arg Asn Phe Gly Leu		
	245	250 255
Tyr Gln Gly Thr Leu Arg Gly Met Met Glu Met Lys Asn Ser His Gln		
	260	265 270
Leu Ile Asp Glu Asn Ile Ile Gly Lys Leu Lys Glu Leu Ala Leu Glu		
	275	280 285
Glu Leu Gly Gly Phe His Gly Lys Asn Ala Glu Leu Met Ser Ser Leu		
	290	295 300
Val Ala Glu Pro Ser Leu Tyr Ala Ala		
305	310	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/21772

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 1/21, 5/14, 5/16, 9/10, 15/29, 15/63; C12P 21/00

US CL : 435/69.1, 193, 243, 320.1, 325, 419; 514/2, 44; 536/23.6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 193, 243, 320.1, 325, 419; 514/2, 44; 536/23.6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, Medline, Biosis, WPIDS
search terms: geranyl diphosphate synthase

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ENDO et al. Demonstration of geranyl diphosphate synthase in several higher plants. Phytochemistry. 1992, Vol. 31, Number 7, pages 2273-2275, especially page 2274.	15-20
X	SUTCLIFFE, J.G. Complete Nucleotide Sequence of the Escherichia coli Plasmid pBR322. Cold Spring Harbor Symposium on Quantitative Biology. 1979, Vol. 43, pages 77-90, especially page 85.	1-7, 9, 10, 12, 13, 23

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

04 JANUARY 1999

Date of mailing of the international search report

02 FEB 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Authorized officer

JOHN S. BRUSCA

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/21772

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 25-29
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/21772

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group 1, claim(s) 1-21 and 37, drawn to genes encoding geranyl diphosphate synthase, geranyl diphosphate synthase protein, and vectors and host cells comprising the gene, and a first method of using the gene consisting of expressing the gene in a cell.

Group 2, claim(s) 30, drawn to a second method of using the gene and proteins of group 1 consisting of introducing geranyl diphosphate protein to a cell.

Group 3, claim(s) 31-33, drawn to a third method of using the gene and proteins of group 1 consisting of using a gene encoding geranyl diphosphate synthase in a method of treating cancer.

Group 4, claim(s) 34-36, drawn to a fourth method of using the gene and proteins of group 1 consisting of using a gene encoding geranyl diphosphate synthase in a method of treating cancer.

The inventions listed as Groups 2-4 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Annex B does not provide for unity of invention between a product and more than one method of using the product.